

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: December 28, 2000, 09:56:08 ; Search time 2435.54 Seconds
(without alignments)
3929.054 Million cell updates/sec

Title: US-08-989-362-1
Perfect score: 2191
Sequence: 1 GCCAGGACCTCTGTGAACCG.....TTTTGGTACTTAAAAATGCC 2191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1033670 seqs, 2183789903 residues 2067340
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	GenEmbl:*			
	1:	gb_ba1:	*	
	2:	gb_ba2:	*	
	3:	gb_om:	*	
	4:	gb_ov:	*	
	5:	gb_pat:	*	
	6:	gb_ph:	*	
	7:	gb_pl1:	*	
	8:	gb_pl2:	*	
	9:	gb_pr1:	*	
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	11:	gb_pr3:	*	
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	13:	gb_sy:	*	
	14:	gb_un:	*	
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	16:	em_hum1:	*	
	17:	em_hum2:	*	
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	19:	em_om:	*	
	20:	em_or:	*	
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	23:	em_ph:	*	
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	25:	em_ro:	*	
	26:	em_sts:	*	
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	32:	gb_in2:	*	
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	34:	gb_pl3:	*	
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90:	gb_htg23:	*
91:	gb_sts1:	*
92:	gb_sts2:	*
93:	gb_v11:	*
94:	gb_v12:	*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
1	2144.8	97.9	2295	5	AR062119	AR062119 Sequence
2	2144.8	97.9	2299	12	AF053713	AF053713 Mus muscu
3	2143.2	97.8	2225	12	AF019048	AF019048 Mus muscu
4	2049.2	93.5	2237	12	AF013170	AF013170 Mus muscu
5	1460.8	66.7	2029	12	AB022036S4	AB022039 Mus muscu
6	1118.8	51.1	2271	11	AF053712	AF053712 Homo sapi
7	1107.8	50.6	2201	11	AF019047	AF019047 Homo sapi
8	957.2	43.7	1823	11	AF013171	AF013171 Homo sapi
9	951	43.4	951	12	AB008426	AB008426 Mus muscu
10	951	43.4	951	12	AB036798	AB036798 Mus muscu
11	818.2	37.3	864	12	AB032771	AB032771 Mus muscu
12	771.8	35.2	205139	85	AL139382	AL139382 Homo sapi

13	726	33.1	754	12	AB03:1772	Mus muscu
14	688.4	31.4	113451	77	AC02:1297	AB03:2772 Homo sapi
15	545.8	24.9	930	77	AC03:7199	AB03:7599 Homo sapi
16	347.4	15.9	764	12	AB02:2036S1	AB02:2036 Mus muscu
17	167.4	7.6	468	12	AB02:2036S2	AB02:2037 Mus muscu
18	105.8	4.8	575	12	AB02:2036S3	AB02:2038 Mus muscu
19	97	4.4	194030	70	AC01:1969	AB01:0969 Homo sapi
20	74.2	3.4	4362	33	DD06:0170	U60170 Dictyostell
21	72.2	3.3	113451	77	AC02:1297	AB03:2772 Homo sapi
22	72	3.3	150754	11	AC02:1491	AC02:2491 Homo sapi
23	72	3.3	175358	10	AC00:7981	AB00:7981 Homo sapi
24	64.8	3.0	1100000	90	PFMA:13P2_2	Continuation (3 of
25	64.2	2.9	94384	11	AC01:1718	AC01:1718 Homo sapi
26	64	2.9	12900	31	AE00:1429	AE00:1429 Plasmodiu
27	63.4	2.9	256172	68	AC00:1319	AC00:5139 Plasmodiu
28	63.2	2.9	13859	31	AE00:1366	AE00:1366 Plasmodiu
29	62	2.8	63282	75	AC02:1756	AC02:0756 Homo sapi
30	62	2.8	160401	69	AC02:1277	AC00:9277 Homo sapi
31	61.2	2.8	182340	75	AC02:1006	AC02:1006 Homo sapi
32	60.8	2.8	1181	34	MSC:X13	X14910 Yeast mitoc
33	60.8	2.8	85779	34	SC00:11856	AC01:1856 Saccharom
34	60.8	2.8	158250	75	AC02:2781	AC02:0781 Homo sapi
35	60.6	2.8	151922	68	AC00:3278	AC00:6278 Plasmodiu
36	60.4	2.8	176552	9	AC00:4317	AC00:4617 Homo sapi
37	60	2.7	151941	70	AC01:5938	AC01:5938 Homo sapi
38	60	2.7	167810	13	AC00:7051	AC00:7051 Homo sapi
39	59.8	2.7	13684	31	AE00:1403	AE00:1403 Plasmodiu
40	59.8	2.7	234112	33	PFMA:4P2	AL035475 Plasmodiu
41	59.6	2.7	2858	34	YSCMTCG38	L36902 Saccharomyc
42	59.6	2.7	12813	33	AE00:1382	AE00:1382 Plasmodiu
43	59.6	2.7	66441	33	PFMAL1P4	AL031747 Plasmodiu
44	59.2	2.7	14867	31	AE00:1398	AE00:1398 Homo sapi
45	59.2	2.7	157016	70	AC01:0948	AC01:0948 Homo sapi

						ALIGNMENTS			
RESULT 1									
AR062119	OCUS	AR062119	2295 bp	DNA	PAT				29-SEP-1999
	SEQUENCE	Sequence 6 from patent US 5843678.							
	AR062119								
	AR062119.1	GI:5989810							
	CYWORDS								
	SOURCE	Unknown.							
	ORGANISM	Unknown.							
	REFERENCE	Unclassified.							
	AUTHORS	Boyle.W.J.							
	TITLE	Osteoprotegerin binding proteins							
	JOURNAL	Patent: US 5843678-A	6 01-DEC-1998;						
	FEATURES	Location/Qualifiers							
	source	1..2295							
		/organism="unknown"							
BASE COUNT	648 a	487 c	538 g	622 t					
ORIGIN									
Query Match	97.9%;	Score 2144.8;	DB 5;	Length 2295;					
Best Local Similarity	99.4%;	Precl. No. 0;							
Matches 2174;	Conservative	0;	Mismatches	12;	Indels	2;	Gaps	2;	
1	GCACGAGCCTCTGTGAACGGTTCGGGX	GGGGGCCCGCCCTGGCCGGAGTCTGCTCGGCGG	60						
34	GCACGAGCCTCTGTGAACGGTTCGGGX	GGGGGCCCGCCCTGGCCGGAGTCTGCTCGGCGG	93						
61	TGGGTGGCCGAGCAAGGAGAGAACAAT	CAGCAGCAGCGGCCCGAACACTCCGGGCGCGG	120						
94	TGGGTGGCCGAGCAAGGAGAGAACAAT	CAGCAGCAGCGGCCCGAACACTCCGGGCGCGG	153						
121	GCACATGGCCCGGCCGAGCCAGACTA	CGCAAGTAGCTGCGCAGCTCGGAGGAGATGGG	180						

Db	154	CGCATGCGCGCGCGCCAGCCAGAGACTACGGGAAGTACCTTGGCGCAGCTCGGAGGAGATGGC	213
Qy	181	CAGGGCCCCGGGCTCCACACGAGGGTCCGCTGCACCCCGCGCCCTTCTGCACCCGGCTCC	240
Db	214	CAGCGCCCCGGGCTCCACACGAGGGTCCGCTGCACCCCGCGCCCTTCTGCACCCGGCTCC	273
Qy	241	GGCGCGCCACCCCGCGCTCCCGCTCCACTGTTCCTGGCGCCCTCCCTGGGCTGGGACTGGG	300
Db	274	GGCGCGCCACCCCGCGCTCCCGCTCCACTGTTCCTGGCGCCCTCCCTGGGCTGGGACTGGG	333
Qy	301	CCAGGTGCTGCGACATCGCTCTGTTCCTGTACTTTTCGAGCGCAGATGGATCCTTAACAG	360
Db	334	CCAGGTGCTGCGACATCGCTCTGTTCCTGTACTTTTCGAGCGCAGATCGATCCTTAACAG	393
Qy	361	AATATCAGAAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTCCATGAAGCGCAGG	420
Db	394	AATATCAGAAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTCCATGAAGCGCAGG	453
Qy	421	TTTTCAGGACTCGACTCTTGGAGAGTGAAGACACACTACTCTGACTCCTGCAGGAGGATGAA	480
Db	454	TTTTCAGGACTCGACTCTGAGAGTGAAGACACACTACTGACTCCTGCAGGAGGATGAA	513
Qy	481	ACAAGCCTTTTCAGGGGGCGGTCGAGAAGAACTGCAACACATTTGGGGCCACAGCGTT	540
Db	514	ACAAGCCTTTTCAGGGGGCGGTCGAGAAGAACTGCAACACATTTGGGGCCACAGCGTT	573
Qy	541	CTCAGGAGCTCCAGCTATGATGGAGGGCTCATGGTTGGATGTGGGCCACGAGGCGCAAGCC	600
Db	574	CTCAGGAGCTCCAGCTATGATGGAGGGCTCATGGTTGGATGTGGGCCACGAGGCGCAAGCC	633
Qy	601	TGAGGGCCAGGCATTTGCGACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCA	660
Db	634	TGAGGGCCAGGCATTTGCGACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCA	693
Qy	661	TAAAGTCACTCTGTCTCTTGGTACCAGATCGAGGCTGGGCGCAAGATCTCTTAACATGAC	720
Db	694	TAAAGTCACTCTGTCTCTTGGTACCAGATCGAGGCTGGGCGCAAGATCTCTTAACATGAC	753
Qy	721	GTTAAGCAACGGAAACTTAAGGTTTAACCAAGATGGCTTCTATTACCTGTACGCCAAGAT	780
Db	754	GTTAAGCAACGGAAACTTAAGGTTTAACCAAGATGGCTTCTATTACCTGTACGCCAAGAT	813
Qy	781	TTGCTTTTCGGCATCATGAACATCGGAAGCGTACCTACAGACTATCTTACGCTCATGGT	840
Db	814	TTGCTTTTCGGCATCATGAACATCGGAAGCGTACCTACAGACTATCTTACGCTCATGGT	873
Qy	841	GTATGTCGTTTAAACACGAGCATCAAAATCCCAAGTTCTCATACCTGTATGAAGGAGGAG	900
Db	874	GTATGTCGTTTAAACACGAGCATCAAAATCCCAAGTTCTCATACCTGTATGAAGGAGGAG	933
Qy	901	CACGAAAACATGGTCGGCAATCTCGAATTCACCTTTTATTCCTAAATGTTGGGGGATT	960
Db	934	CACGAAAACATGGTCGGCAATCTCGAATTCACCTTTTATTCCTAAATGTTGGGGGATT	993
Qy	961	TTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTTACGCTGTCCCAACCTTCCCTGCTGGA	1020
Db	994	TTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTTACGCTGTCCCAACCTTCCCTGCTGGA	1053
Qy	1021	TCCGGATCAAGATCGGACGTAATTTGGGGCTTTCAAAGTTCAGGACATAGACTGAGACTC	1080
Db	1054	TCCGGATCAAGATCGGACGTAATTTGGGGCTTTCAAAGTTCAGGACATAGACTGAGACTC	1113
Qy	1081	ATTTTCGTTGGAACATTAGCATGGATGCTCTAGATGTTTGGAAACTTCTTAAAAAATGGATG	1140
Db	1114	ATTTTCGTTGGAACATTAGCATGGATGCTCTAGATGTTTGGAAACTTCTTAAAAAATGGATG	1173
Qy	1141	ATGTCCTATACATGTTGAAGACTACTTAAGACATATGGCCACCGGCTATGAACATCACAGC	1200
Db	1174	ATGTCCTATACATGTTGAAGACTACTTAAGACATATGGCCACCGGCTATGAACATCACAGC	1233
Qy	1201	CCTCTCTCTGAGCGCTGTACAGTTTGTGTATATGTAAAGTCCATAGGTGATGTTTAGATTC	1260
Db	1234	CCTCTCTCTGAGCGCTGTACAGTTTGTGTATATGTAAAGTCCATAGGTGATGTTTAGATTC	1293

QY	1261	ATGGTGATTACACAACGGTTTTACAAATTTTCTAAATGATTTTCCTTAAGAAATTTGAACCCAGATT	1320
DB	1294	ATGGTGATTACACAACGGTTTTACAAATTTTGTAAATGATTTCTCT - AGAAATTTGAACCCAGATT	1352
QY	1321	GGGACAGGTATTTCCGATGCTTATGAAAACCTTACACGCTGAGCTATGCAAGGGGGTCCACAG	1380
DB	1353	GGGACAGGTATTTCCGATGCTTATGAAAACCTTACACGCTGAGCTATGGAAGGGGGTCCACAG	1412
QY	1381	TCTCTGGGTCTAACCCCTGGACATGTGCCACTGAGAACCTTGAAATTAAGAAGATGCCAT	1440
DB	1413	TCTCTGGGTCTAACCCCTGGACATGTGCCACTGAGAACCTTGAAATTAAGAAGATGCCAT	1472
QY	1441	GTCAATTGCAAGAAATGATAGTGTGAAGGGTTAAGTTCCTTTTGAAATTTGTACATTCGGCT	1500
DB	1473	GTCAATTGCAAGAAATGATAGTGTGAAGGGTTAAGTTCCTTTTGAAATTTGTACATTCGGCT	1532
QY	1501	GGGACCTGCAAAATAGTTCCTTTTCTTAATCAGGAGAGAAAATATATATCTATTTTTATA	1560
DB	1533	GGGACCTGCAAAATAGTTCCTTTTCTTAATCAGGAGAGAAAATATATATCTATTTTTATA	1592
QY	1561	TAAATGCTCAAAGTTATATTTCAGGTGTAATGTTTCTGTGCAAGGTTTTGTAAATTTATAT	1620
DB	1593	TAAATGCTCAAAGTTATATTTCAGGTGTAATGTTTCTGTGCAAGGTTTTGTAAATTTATAT	1652
QY	1621	TTGTGCTATAGTATTTTGAATTCAAAATATTTTAAAAATGCTCTACTGTTGCATATTTTAAATG	1680
DB	1653	TTGTGCTATAGTATTTTGAATTCAAAATATTTTAAAAATGCTCTACTGTTGCATATTTTAAATG	1712
QY	1681	TTTTTAAATGTCACAGATGATTTAACTGGGHCACCTTTGTAAATTCCTCCCTGAAGGTAATCGTA	1740
DB	1713	TTTTTAAATGTCACAGATGATTTAACTGGGHCACCTTTGTAAATTCCTCCCTGAAGGTAATCGTA	1772
QY	1741	GCTAAGGGGGCAGAACTGTTCTGTTGTCACCACATGTAAGTTATTTCTTTTATCTCTTTT	1800
DB	1773	GCTAAGGGGGCAGAACTGTTCTGTTGTCACCACATGTAAGTTATTTCTTTTATCTCTTTT	1832
QY	1801	AACTTAATAGAGTCCTCAGACTTGTCAAAACATGTCGAAGCAAAATAAATAAATAAATAAATA	1860
DB	1833	AACTTAATAGAGTCCTCAGACTTGTCAAAACATGTCGAAGCAAAATAAATAAATAAATAAATA	1892
QY	1861	AAATGAATATCTTGAATTAATAGTAGGATTTGGTCACCAGTGCTCTTCAAAATTTAGAA	1920
DB	1893	AAATGAATACCTTGAATTAATAGTAGGATTTGGTCACCAGTGCTCTTCAAAATTTAGAA	1952
QY	1921	GCTAATTCACCTTTAGGAGCTGACATAGCCAAAAGGATACATAATAGGCTACTGAAAATC	1980
DB	1953	GCTAATTCACCTTTAGGAGCTGACATAGCCAAAAGGATACATAATAGGCTACTG - AAATC	2011
QY	1981	TGTCAGGAGTATTTATGCAATTAATGAACAGGTGCTTTTACAAAGAGCTACAAATTTG	2040
DB	2012	TGTCAGGAGTATTTATGCAATTAATGAACAGGTGCTTTTACAAAGAGCTACAAATTTG	2071
QY	2041	TAAATTTGTTCTCTTTTTCCTCCCATGAAAATGTAATACGTTTATCAGCCAAAAAACA	2100
DB	2072	TAAATTTGTTCTCTTTTTCCTCCCATGAAAATGTAATACGTTTATCAGCCAAAAAACA	2131
QY	2101	ATCCACCTTTTAAATTTAGTGAAGTATTTTATTTACTGTACAAATAAAGCATTTGTTTC	2160
DB	2132	ATCCACCTTTTAAATTTAGTGAAGTATTTTATTTACTGTACAAATAAAGCATTTGTTTC	2191
QY	2161	TGAATGGCATTTTTCGTTTACCTTAAAT	2188
DB	2192	TGAATGGTAAATTTTTCGTTTACAAAAAT	2219

RESULT	2
AF053713 .	
LOCUS	2299 bp mRNA
DEFINITION	Mus musculus osteoprotegerin ligand mRNA, complete cds.
ACCESSION	AF053713
VERSION	AF053713.1 GI:3057147
KEYWORDS	

SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2299)
AUTHORS	Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R., Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S., Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A., Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J., Delaney,J. and Boyle,W.J.
TITLE	Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation
JOURNAL	Cell 93 (2), 165-176 (1998)
MEDLINE	98227661
REFERENCE	2 (bases 1 to 2299)
AUTHORS	Boyle,W.J.
TITLE	Direct Submission
JOURNAL	Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc., One Amgen Center Drive, Thousand Oaks, California 91320, USA
FEATURES	Location/Qualifiers
source	1. .2299
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CDS	170..1120
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	/protein_id="AAC40113.1"
	/db_xref="GI:3057148"
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BASE COUNT	641 a 494 c 541 g 623 t
ORIGIN	

Query Match	97.9%	Score 2144.8	DB 12	Length 2299
Best Local Similarity	99.4%	Pred. No. 0		
Matches 2174	Conservative 0	Mismatches 12	Indels 2	Gaps 2
QY 1	GCACAGACCTCTGTGAACCGTTCGGGCGGGGGCCGCTTGGCCGGAGTCTGCTCGGCGG 60			
DB 46	GCACGACCTCTGTGAACCGTTCGGGCGGGGGCCGCTTGGCCGGAGTCTGCTCGGCGG 105			
QY 61	TGGTGGCCGAGGAAGGAGAACGATTCGCGAGCAGGCGGCCCAACTCCGGGGGCCG 120			
DB 106	TGGTGGCCGAGGAAGGAGAACGATTCGCGAGCAGGCGGCCCAACTCCGGGGGCCG 165			
QY 121	CGCCATCGCCGGGCCAGCGAGACTACGCAAGTACTCGCAGACTCGAGAGAGATGGG 180			
DB 166	CGCCATCGCCGGGCCAGCGAGACTACGCAAGTACTCGCAGACTCGAGAGAGATGGG 225			
QY 181	CAGGGCCCGGGGTCCACACAGAGGTTCGCTGCACCCCGCGCTTCTGCACCGGTCC 240			
DB 226	CAGGGCCCGGGGTCCACACAGAGGTTCGCTGCACCCCGCGCTTCTGCACCGGTCC 285			
QY 241	GGCGCCGACCGCCGCGCTCCCGCTCCATGTCCTGGCCCTCTCTGGGGCTGGGACTGG 300			
DB 286	GGCGCCGACCGCCGCGCTCCCGCTCCATGTCCTGGCCCTCTCTGGGGCTGGGACTGG 345			
QY 301	CCAGTGGTCTGCAGCATCGCTCTGTTCTGTACTTTTCGAGCGCAGATGGATCCTAACAG 360			
DB 346	CCAGTGGTCTGCAGCATCGCTCTGTTCTGTACTTTTCGAGCGCAGATGGATCCTAACAG 405			
QY 361	AATATCAGAGACGAGCTACTGCTTTTATAGAACTCTGAGACTCCATGAAACGCGAGG 420			
DB 406	AATATCAGAGACGAGCTACTGCTTTTATAGAACTCTGAGACTCCATGAAACGCGAGG 465			
QY 421	TTTTCGAGGACTCTGAGTCTGGAGACTGAAGACACTACCTGACTTCCTGCGAGGAGTAA 480			

Db 466 TTTTGCAGGACTCGACTCTGAGAGTGAAG:ACACACTACCTGACTCTCTGCAGGAGGATGAA 525
QY 481 ACAAGCCCTTCAGGGGCCGTGCAAG:AACTGCAACACATGTTGGGGCCACAGCGCTT 540
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Db 586 CTCAGGAGCTCCAGCTATGATGAGGCG:CATGGTTGGATGTTGGCCCGAGGAGCAAGCC 645
QY 601 TGAGGCCAGCCATTTTCACACACCTCAC:ATCAATGCTGCCAGCATCTCCATCGGGTCCCA 660
Db 646 TGAGGCCAGCCATTTTCACACACCTCAC:ATCAATGCTGCCAGCATCTCCATCGGGTCCCA 705
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QY 841 GTATGCTGTTTAAACACAGCATCAAAATC:CAAGTTCTCATAACTGATGAAGGAGGAG 900
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QY 901 CAGCAAAACTGTCGGGCAATTTCTGAATTC:CAACTTTTATTCCTAAATGTTGGGGGATT 960
Db 946 CAGCAAAACTGTCGGGCAATTTCTGAATTC:CAACTTTTATTCCTAAATGTTGGGGGATT 1005
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QY 1021 TCCGGATCAAGATCGGACGTACTTTGGG:CTTTCAAAAGTTTCAGGACATAGACTGAGACTC 1080
Db 1066 TCCGGATCAAGATCGGACGTACTTTGGG:CTTTCAAAAGTTTCAGGACATAGACTGAGACTC 1125
QY 1081 ATTTCTGGGAACATAGCATGGATGTCCTAGATGTTGGAAACTTTTAAATAATGATG 1140
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RESULT 3
AF019048
LOCUS
DEFINITION Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, complete cds.
ACCESSION AF019048
VERSION AF019048.1 GI:2612923
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2225)
AUTHORS Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C., Tomesko,M.E., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and Galibert,L.
TITLE A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function
JOURNAL Nature 390 (6656), 175-179 (1997)
MEDLINE 98032977
REFERENCE 2 (bases 1 to 2225)
AUTHORS Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E., Cosman,D., Dubose,R. and Galibert,L.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51 University St., Seattle, WA 98101, USA

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Best Local Similarity	99.3%;	Pred. No. 0;
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DB	73	TGGGTGCGCGAGGAAGGAGAGAACGATCGCGGAGCAGGGCGGCCCGAACTCCGGGCGCG 132
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QY	181	CAGCGGCCCGGGCTCCACACAGAGGTTCGCTGCACCCCGCGCTTCTGCACCGGCTCC 240
DB	193	CAGCGGCCCGGGCTCCACACAGAGGTTCGCTGCACCCCGCGCTTCTGCACCGGCTCC 252
QY	241	GGCGCGGCCACCGCGCGCTCCCGCTCCATGTTCTTGGCGCTTCTGGGCTGGGACTGGG 300
DB	253	GGCGCGGCCACCGCGCGCTCCCGCTCCATGTTCTTGGCGCTTCTGGGCTGGGACTGGG 312
QY	301	CCAGGTGGTCTGCAGCATCGCTCTGTTCCTGTACTTTTCGAGCGCAGATGGATCTAACAG 360
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QY	361	AATATCAGAAGACAGCACTCACTGCTTTTATAGAATCCTTGAGACTCCTGAAACCGCAGG 420
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QY	481	ACAAGCCCTTCAGGGGGCGTGCAGAAAGACTGCAACACATTTGTGGGGCCACAGCGCTT 540
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DB	673	TAAAGTCACTCTGTCTCTTGGTACCACGATCGAGGCTGGCCAAAGATCTCTTACATGAC 732
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RESULT 4
AF013170
LOCUS AF013170 2237 bp mRNA ROD 05-NOV-1998
DEFINITION Mus musculus TNF-related ligand TRANCE mRNA, complete cds.
ACCESSION AF013170
VERSION AF013170.1 GI:2411497
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2237)
Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlicki,J., Chao,M.,
Kalachikov,S., Cayani,E., Bartlett,F.S. III, Frankel,W.N., Lee,S.Y.
and Choi,Y.
TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
97460112
2 (bases 1 to 2237)
Wong,B.R., Josien,R., Lee,S.Y., Sauter,B., Li,H.L., Steinman,R.M.
and Choi,Y.
TRANCE (tumor necrosis factor [TNF]-related activation-induced
cytokine), a new TNF family member predominantly expressed in T
cells, is a dendritic cell-specific survival factor
J. Exp. Med. 186 (12), 2055-2080 (1997)
98060869
3 (bases 1 to 2237)
Fuller,K., Wong,B., Fox,S., Choi,Y. and Chambers,T.J.
TRANCE is necessary and sufficient for osteoblast-mediated
activation of bone resorption in osteoclasts
J. Exp. Med. 188 (5), 997-1001 (1998)
98401035
4 (bases 1 to 2237)
Wong,B.R., Josien,R., Lee,S.Y., Vologodskaya,M., Steinman,R.M. and
Choi,Y.
The TRAF family of signal transducers mediates NF-kappaB activation
by the TRANCE receptor
J. Biol. Chem. 273 (43), 28355-28359 (1998)
98447691
5 (bases 1 to 2237)
Wong,B.R., Rho,J., Arron,J., Robinson,E. and Choi,Y.

TITLE Direct Submission
JOURNAL Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA
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Best Local Similarity 98.4%; Pred. No. 0;
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LOCUS	AB022036S4	2029 bp	DNA
DEFINITION	Mus musculus DNA for osteoclast differentiation factor, exon 5, complete cds.		
ACCESSION	AB022039.1	GI:4127268	
VERSION	AB022039.1		
KEYWORDS	osteoclast differentiation factor.		
SEGMENT	4 of 4		
SOURCE	Mus musculus (strain:129) embryonic stem cell DNA.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (sites)		
	Kodaira,K., Kodaira,K., Mizuno,A., Yasuda,H., Shima,N., Murakami,A., Ueda,M. and Higashio,K.		
TITLE	Cloning and characterization of the gene encoding mouse osteoclast differentiation factor		
JOURNAL	Gene 230 (1), 121-127 (1999)		
MEDLINE	99214075		
REFERENCE	2 (bases 1 to 2029)		
AUTHORS	Kodaira,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-JAN-1999) to the DDBJ/EMBL/GenBank databases		
	Kunihiko Kodaira, YS New Technology Institute Inc., Molecular Biology, Shimoishibashi 519, Ishibashi-machi, Tohigi 329-0512, Japan (E-mail:Y.S.NT@et-cnet.or.jp, Tel:81-285-52-2821, Fax:81-285-52-2824)		
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QY 713 AACATGACGTTAAGCAACGAAACTAA:IGTTAAACCAAGATGGCTTCTATTACCTGTAC 772
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AF053712 2271 bp mRNA PRI 09-MAY-1998
LOCUS Homo sapiens osteoprotegerin ligand mRNA, complete cds.
DEFINITION AF053712
ACCESSION AF053712.1 GI:3057145
VERSION
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2271)
AUTHORS Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R.,
Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S.,
Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A.,
Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J.,
Delaney,J. and Boyle,W.J.

TITLE Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2271)
AUTHORS Boyle,W.J.
TITLE Direct Submission

JOURNAL	Submitted (16-WAR-1998)	Department of Cell Biology, Amgen, Inc., One Amgen Center Drive, Thousand Oaks, California 91320, USA
FEATURES	Location/Qualifiers 1..2271	
source	/organism="Homo sapiens" /db_xref="taxon:9606"	
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DEFINITION (RANKL) mRNA, complete cds.
ACCESSION AF019047
VERSION AF019047.1 GI:2612921
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SOURCE Homo sapiens
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REFERENCE 1 (bases 1 to 2201)
AUTHORS Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
Tometsko,M.E., Roux,E.R., Teepe,M.C., DuBose,R.F., Cosman,D. and
Galibert,L.
TITLE A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
JOURNAL Nature 390 (6556), 175-179 (1997)
MEDLINE 98032977
AUTHORS Cosman,D., DuBose,R. and Galibert,L.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA, 98101, USA
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RESULT 8
AF013171 LOCUS AF013171 1823 bp mRNA PRI 19-SEP-1997
DEFINITION Homo sapiens TNF-related ligand TRANCE mrna, partial cds.
ACCESSION AF013171
VERSION AF013171.1 GI:2411499
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1823)
AUTHORS Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlinick,J., Chao,M.,
Kalachikov,S., Cayani,E., Bartlett,F.S. III, Frankel,W.N., Lee,S.Y.
and Choi,Y.
TITLE TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
MEDLINE 97460112
REFERENCE 2 (bases 1 to 1823)
AUTHORS Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
Direct Submission
TITLE Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA
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BASE COUNT 569 a 305 c 380 g 569 t
ORIGIN

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Db	1520	AGGATGTTGGCCACCCAGGTGCTTTCAAAATTTAGAGAGCTAATTTGACTTTAGAGAGCTGAC	1579
QY	1944	ATAGCCAAAAGGATACATAATAGGTACTGAAAAATCTGTCCAGGAGTATTTATGCAATTA	2003
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QY	2184	AA 2185	
Db	1810	AA 1811	
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LOCUS	951 bp	mRNA	02-MAY-1998
DEFINITION	Mus musculus mRNA for osteoclast differentiation factor (ODF), complete cds.		
ACCESSION	AB008426		
VERSION	AB008426.1	GI:3041781	
KEYWORDS	osteoclast differentiation factor (ODF).		
SOURCE	Mus musculus bone marrow stromal cells clone.lib:pcDL-SRa296 clone:pOBM291.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
AUTHORS	Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 951)		
JOURNAL	Yasuda.H.		
	Direct Submission		
	Submitted (22-OCT-1997) to the DDBJ/EMBL/GenBank databases.		
	Hisataka Yasuda, Snow Brand Milk Products Co., Ltd., Research		
	Institute of Life Science, 519 Shimo-Ishibashi, Ishibashi-machi,		
	Tochigi 329-05, Japan (E-mail:fvb7042@mb.infoweb.or.jp).		
REFERENCE	Tel:0285-52-1331, Fax:0285-53-1314		
	2 (sites)		

AUTHORS Yasuda,H., Shima,N., Nakagawa,N., Yamaguchi,K., Kinoshita,M., Mochizuki,S., Tomoyasu,A., Iano,K., Goto,M., Murakami,A., Tsuda,E., Morinaga,T., Higashio,K., Udagawa,N., Takahashi,N. and Suda,T.

TITLE Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998)

MEDLINE 98186248

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BASE COUNT 231 a 267 c 248 g 205 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4e-166;

Matches 951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 245 CGGCCACCGCGCGCTCCCGCTCCATGTTCTGCGCCCTCTGCGGCTGGGACTGGGCGAG 304

Db 121 CGGCCACCGCGCGCTCCCGCTCCATGTTCTGCGCCCTCTGCGGCTGGGACTGGGCGAG 180

QY 305 GTGGTCTGCAGACGCTGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 364

Db 181 GTGGTCTGCAGACGCTGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 240

QY 365 TCAGAAGACAGCACTACTGCTTTTATAGAACTCTGAGACTCCATGAAGAACGAGGTTTG 424

Db 241 TCAGAAGACAGCACTACTGCTTTTATAGAACTCTGAGACTCCATGAAGAACGAGGTTTG 300

QY 425 CAGGACTCGACTCTGGAGAGTGAAGACACACTACTGCTGACTCTCTGAGGAGGATGAACAA 484

Db 301 CAGGACTCGACTCTGGAGAGTGAAGACACACTACTGCTGACTCTCTGAGGAGGATGAACAA 360

QY 485 GCCTTTTCAGGGCGGCTGCGAGAGGAATCTGACACACTGTTGGGGCCACAGCGCTTCTCA 544

Db 361 GCCTTTTCAGGGCGGCTGCGAGAGGAATCTGACACACTGTTGGGGCCACAGCGCTTCTCA 420

QY 545 GGAGCTCCAGCTATGATGGAAGGCTCATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 604

Db 421 GGAGCTCCAGCTATGATGGAAGGCTCATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 480

QY 605 GCCCAGGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCATAAA 664

Db 481 GCCCAGGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCATAAA 540

QY 665 GTCACCTGCTCTCTTGTGTACACGATCGAGCTGGGGCCAAAGATCTCTTAACATGAGCTTA 724

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QY 905 AAAAAGTGGTGGGCAATCTCAATCCACTTTTATTCATAAATGCTTGGGGATTTTC 964

Db 781 AAAAAGTGGTGGGCAATCTCAATCCACTTTTATTCATAAATGCTTGGGGATTTTC 840

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QY 1025 GATCAAGATGCCACCTACTTTGGGCTTTCAAAGTTCAGGACATAGACTGA 1075

Db 901 GATCAAGATGCCACCTACTTTGGGCTTTCAAAGTTCAGGACATAGACTGA 951

RESULT 10

AB036798 951 bp mRNA ROD 29-JUN-2000

LOCUS Mus musculus mRNA for RANKL 1, complete cds.

DEFINITION AB036798

ACCESSION AB036798.1 GI:8843829

VERSION AB036798.1

KEYWORDS RANKL 1.

SOURCE Mus musculus cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 951)

AUTHORS Ikeda,T.

TITLE RANKL 1

JOURNAL Published Only in Database (2000) In press

REFERENCE 2 (bases 1 to 951)

AUTHORS Ikeda,T.

TITLE Direct Submission

JOURNAL Submitted (11-JAN-2000) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)

FEATURES

source Location/Qualifiers

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BASE COUNT 231 a 267 c 248 g 205 t

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Query Match 35.2%; Score 771.8; DB 85; Length 205139;
Best Local Similarity 76.3%; Pred. No. 2.2e-133;
Matches 1190; Conservative 0; Mismatches 302; Indels 67; Gaps 17;

Qy 643 CATCCATCGGTTCCCATAAAGTCACCTCTGTCCTCTTGGTACCACGATCGAGGCTGGGC 702
Db 135083 CTTCTCCACAGGTTCCCATAAAGTAGTCTGTCCTCTTGGTACCACGATCGGCGGTGGGC 135142

Qy 703 CAAGATCTCTAACATGACGTTAAAGCAACGGAACAACTAAAGGTTTAAACAGATGGGCTTCTA 762
Db 135143 CAAGATCTCCACATGACCTTTTAGCAATGGAAACTATAGTAAATCAGGATGGCTTTTA 135202

Qy 763 TTACCTGTACGCCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGA 822
Db 135203 TTACCTGTATGCCAACATTTGCTTTCGACATCATGAACTTCAGGAGACCTAGCTACAGA 135262

Qy 823 CTATCTTCAGCTGATGGTGTATGTCGTTTAAACACAGCATCAAAATCCCAAGTCTCATAA 882
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Qy 883 CCTGATGAAAGGAGGAGCAGCAAAAACCTGTCGGGCAATCTGAATTCCTACCTTTTATTC 942
Db 135323 CCTGATGAAAGGAGGAGCAGCAAACTATTGGTCAGGGAATTTCTGAATTTCCATTTTATTC 135382

Qy 943 CATAAATGTTGGGGATTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGTC 1002
Db 135383 CATAAAGTGTGTTGATTTTAAAGTTACGGTCTGGAGAGAAATCAGCATCGAGGTCTC 135442

Qy 1003 CAACCCCTCCCTGCTGGATCCGATCAAGATGCGACGACTTTGGGGCTTTCAAAAGTTCA 1062
Db 135443 CAACCCCTCCCTTACTGGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTCCG 135502

Qy 1063 GGACATAGACTGACACTCATTTTCGTGGACATTAGCATGGATGCTCAGATGTTTGGAAA 1122
Db 135503 AGATATAGATTGAGCCCCAGTTTGGAGTGT---ATGTAATTCCTGGATGTTTGGAAA 135559

Qy 1123 CTTCTTAAAAA-----ATGGATGATGCTCATACATGTAAGACTACTAAGACACATG 1175
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Qy 1355 ACGTGAGCTATGGAAGGGGGTGCACAGTCTCTGGGCTCAACCCCTGGACATGTGCCACTGA 1414
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Qy 1415 GAACCTTGAAATTAAGAAAGATGCCATGTCATTGCAAGAAATGATGATGTGAAGGTTAA 1474
Db 135843 GCAGC-TGAAGTGGAGAGGGGTGTCATCT-AGCGCAATTTGAAGGATCATCTGAAGGGGCAA 135900

Qy 1475 GTTCTTTTGAATTTGATGTCGCTGGAGCTGCAAAATAGTCTTTTTTCTCAATGAG 1534
Db 135901 ATCTTTTGAATTTGTTACATCATCATCTGGAACTGCCAAAAATAC---TTTTTCTAATGAG 135957

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Db 136017 TCTTTGCAAAAGTATTGTAAATTTATATTTTGTCTATAGTATTTTGTATTTCAAAATATTTAAA 136076
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Qy	1655	ATGTCACACTGTTGCACATATTTAAATGTTTAAATGTCACAGATGTATTTAACTGGTGCACT	1714
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Qy	1715	TTGTAATTCCTCCCTG- ---AAGTACTCGTAGCTAAGGGGCGAGATACTGTTTCTGGTG	1769
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Qy	1770	ACCACATGTAGTTATTTCTTTTAACTTAATAGAGTCTTTCAGACTTTGTCAA	1828
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Qy	1829	AACATGTCAGACGAAAAATAATAATAAATAAATCAATATCTTGAATAAAGTAGGA	1888
Db	136257	GCCTGTGC- -----AAAAAAATTAATAATGGATGCTTGAATAAAGCAGGA	136302
Qy	1889	TGTTGGTCCACAGGTGCTTTCAAAATTTAGAGCTAATTTGACTTTAG- GAGCTGACATAG	1947
Db	136303	TGTTGGCCACAGGTGCTTTCAAAATTTAGAAACTAATTTGACTTTAGAAGCTGCATATG	136362
Qy	1948	CCAAAAGGATACATATAGGCTACTGACAAAATCTGTGCAGGAGTATTTATGCAATATTGA	2007
Db	136363	CCAAAAGGATACATATAGGGCCACTG- AAATCTGTCAAGAGTAGTATATAATTTGTTGA	136421
Qy	2008	ACAGGTGCTGTTTTTTTACAAGAGCTACAAATTCGTAATTTTGTCTTTTTTTTCCCAT	2067
Db	136422	ACAGGTG- TTTTCCCAAGTGCCGCAATATGACTCTT- ----TTTGTTTTTTTCAAA	136473
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RESULT 13

AB032772 754 bp mRNA ROD 29-JUN-2000
LOCUS Mus musculus RANKL 3 mRNA for receptor activator of NF-kB ligand 3 complete cds.
ACCESSION AB032772
VERSION AB032772.1 GI:8843824
KEYWORDS receptor activator of NF-kB ligand 3.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Ikeda,T., Takahashi,H. and Hirokawa,K.
Somatostatin, a new marker of osteoblast, regulates the expression of RANKL isoforms
Unpublished (1999)
2 (bases 1 to 754)
Ikeda,T.
Direct Submission
Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pch2med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
Location/Qualifiers
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BASE COUNT
ORIGIN

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Query Match	33.18;	Score 726;	DB 12;	Length 754;
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Db 29	GATCCTAACCAATATCAGAAAGACAGCAGCTCACCTGCTTTTATAGAAATCCTGAGACTCCAT	88		
Qy 410	GAACACGCGAGTTTGCAGGACTTCGACTCTGAGAGAGTGAAGACACACTACCTGACTCCTGC	469		
Db 89	GAACACGCGAGTTTGCAGGACTTCGACTCTGAGAGAGTGAAGACACACTACCTGACTCCTGC	148		
Qy 470	AGGAGATGAACAAGCCTTTTCAGGGGCCCTGAGAAAGAACTGCAACACATTTGTGGGG	529		
Db 149	AGGAGATGAACAAGCCTTTTCAGGGGCCCTGAGAAAGAACTGCAACACATTTGTGGGG	208		
Qy 530	CCACAGCGCTTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGGTGGATCTGGCCCCAG	589		
Db 209	CCACAGCGCTTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGGTGGATCTGGCCCCAG	268		
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Qy 650	TCGGTTTCCCAATAAGTCACTCTGTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATC	709		
Db 329	TCGGTTTCCCAATAAGTCACTCTGTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATC	388		
Qy 710	TCTACATGACGTTTAAGCAACGGAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTG	769		
Db 389	TCTACATGACGTTTAAGCAACGGAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTG	448		
Qy 770	TACGCCAACATTTGCTTTTCGGCATCATCAACATCGGGAGCGTACCTACAGACTATCTT	829		
Db 449	TACGCCAACATTTGCTTTTCGGCATCATCAACATCGGGAGCGTACCTACAGACTATCTT	508		
Qy 830	CAGCTGATGGTGTATGTCGTTTAAACACGAGCATCAAAATCCCAAGTTCTCATAACTGATG	889		
Db 509	CAGCTGATGGTGTATGTCGTTTAAACACGAGCATCAAAATCCCAAGTTCTCATAACTGATG	568		
Qy 890	AAAGAGGGAGCAGCAAAACTGCTCGGGCAATTTCTGAATTTCCACTTTTATCCATAAT	949		
Db 569	AAAGAGGGAGCAGCAAAACTGCTCGGGCAATTTCTGAATTTCCACTTTTATCCATAAT	628		
Qy 950	GTTGGGGGATTTTCAAGCTCCGAGCTCGTCAAGAAATTTAGCATTCAGGTTCCAAACCT	1009		
Db 629	GTTGGGGGATTTTCAAGCTCCGAGCTCGTCAAGAAATTTAGCATTCAGGTTCCAAACCT	688		
Qy 1010	TCCCTGCTGGATCCGGATCAAGATCGACGCTACTTTTGGGGCTTTTCAAAAGTTCAGGACATA	1069		
Db 689	TCCCTGCTGGATCCGGATCAAGATCGACGCTACTTTTGGGGCTTTTCAAAAGTTCAGGACATA	748		
Qy 1070	GACTGA 1075			
Db 749	GACTGA 754			
RESULT 14	AC023297/c			
LOCUS	AC023297	113451 bp	DNA	HTG
DEFINITION	Homo sapiens clone RP11-21H9, WORKING DRAFT SEQUENCE, 13 unordered			
ACCESSION	AC023297			
VERSION	AC023297.3	GI:7144965		

RESULT 14
AC023297/C
LOCUS
DEFINITION
ACCESSION
VERSION

HTG 03-MAR-2000
RAFT SEQUENCE, 13 unordered


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Db 12512 GTATCTTCAACTAATGGTGACGTCCTAAACACGACATCAAAATCCCAAGTTCCTCATAC 12453
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QY 943 CATAAATGTTGGGGATTTTTCAGCTCCGAGCTGGTGAAGAAATTAAGCATTCAGGTGTC 1002
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Db 12155 GCGCAACGGTACACGACTCAGTATCCATCTGCTTGACCTGTGTAGAGAACACGGGTATTT 12096
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QY 1236 AAGTCCATAGGTGATGTATGATTCATGGTG-ATTACACACGGTTTTTACAAATTTGTAA 1294
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Db 12095 ACAGCAGTGGGAGATGTTAGACTCATGGTGTGTACACAAATGGTTTTTAAATTTGTAA 12036
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QY 1355 ACCTGAGCTATGAAGGGGCTCACAGTCTCTGGGTCTTAACCCCTGGACATGTGCCACTGA 1414
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Db 11874 ATTCTTTTGAATTTGATACATGCTGTGGAACCTGCAAAAATAC---TTTCTTAATGAG 11818
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QY 1535 GAGAGAAAATATATGATTTTATATAATGCTCTAAAGTTTATATTTTCAGGTGTAATGTTT 1594
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QY 1595 TCTGTGCAAGTTTGTAAATATATTTTGTGCTATAGTATTTGATTCAAATATTTTAAA 1654
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QY 1770 ACCACATGAGTTTATTTCTTTTCTTTTAACTTAAATAGA-GTCTTTCAGACTGTGCAA 1828
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Db 11578 ATCAATGCAAGTATATTTCTTCATCTTTTAAAGTTAATAGATTTTTCAGACTGTGCAA 11519
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RESULT 15

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LOCUS Homo sapiens mRNA for sODF/TRANCE, complete cds.
DEFINITION AB037599
ACCESSION AB037599
VERSION AB037599.1 GI:5863047
KEYWORDS sOdf/trance; SODF/TRANCE.
SOURCE Homo sapiens male tongue epithelial-like squamous cell carcinoma
cell_line:SCC-4 cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Nagai,M., Kyakumoto,S. and Sato,N.
TITLE Cancer cells responsible for humoral hypercalcemia express mRNA
encoding a secreted form of ODF/TRANCE that induces osteoclast
formation
JOURNAL Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)
MEDLINE 20175237
REFERENCE 2 (bases 1 to 930)
AUTHORS Nagai,M., Kyakumoto,S. and Sato,N.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) to the DDBJ/EMBL/GenBank databases.
Masazumi Nagai, Iwate Medical University School of Dentistry,
Department of Biochemistry; 19-1 Uchimaru, Morioka, Iwate 020-8505,
Japan (E-mail:mnagai@iwate-med.ac.jp, Tel:+81-19-651-5111(ex.4436),
Fax:+81-19-654-4147)
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BASE COUNT 283 a 184 c 200 g 260 t 3 others
ORIGIN
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Query Match 24.9%; Score 545.8; DB 9; Length 930;
Best Local Similarity 80.7%; Pred. No. 1.7e-91;
Matches 680; Conservative 0; Mismatches 147; Indels 16; Gaps 3;
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Db 91 GCAGATGATCTCTTAAGAAATATCAGACAGATGCACTGCACTTATAGAAATTTTGG 150
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2000, 17:45:45 ; Search time 109.14 Seconds
(without alignments)
7541.478 Million cell updates/sec

Title: US-08-989-362-1
Perfect score: 2191
Sequence: 1 GCCAGGACCTGTGTACCG.....TTTGGTACTTAATAATGCC 2191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database 1:			
N_Geneseq_36.*			
1:	/cgn2_2/gcgdata/geneseq/geneseq/NA1980.DAT.*		
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21:	/cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	2191	100.0	2191	19 V41489	Nucleotide sequenc
2	2144.8	97.9	2295	19 V70284	Human osteoprotege
3	2144.8	97.9	2299	21 299966	DNA encoding a mur
4	2049.2	93.5	2237	20 X80224	Murine TRANCE enco
5	1615.8	73.7	1630	19 V41377	NF-kB receptor act
6	1615.8	73.7	1630	19 V41371	NF-kB receptor act
7	1525.4	69.6	1538	19 V69886	Nucleic acid encod
8	1118.8	51.1	2271	21 299964	DNA encoding a hum
9	1118.8	51.1	2274	19 V70285	Human osteoprotege
10	957.2	43.7	1823	20 X80223	Human TRANCE encod
11	951	43.4	951	19 V69900	Nucleotide sequenc
12	951	43.4	951	21 299965	DNA encoding a mur

13	951	43.4	951	21	249024	Osteoclast formati
14	735	33.5	735	19	V69898	Nucleic acid encod
15	666.2	30.4	954	19	V41378	NF-kB receptor act
16	666.2	30.4	954	19	V41372	NF-kB receptor act
17	663	30.3	954	19	V69887	Nucleic acid encod
18	519	23.7	741	19	V69899	Nucleic acid encod
19	313.2	14.3	564	21	299967	DNA encoding a syn
20	312.2	14.2	519	21	299968	DNA encoding a syn
21	312.2	14.2	519	21	299969	DNA encoding a mur
22	278.6	12.7	519	21	299972	DNA encoding osteo
23	262.4	12.0	546	21	299971	DNA encoding osteo
24	259.4	11.8	519	21	299973	DNA encoding osteo
25	247.6	11.3	564	21	299970	DNA encoding osteo
26	120.6	5.5	254	20	X56001	Human tumour necro
27	58.4	2.7	846	19	V42205	TNF-related apopto
28	58.4	2.7	1042	18	T72796	Novel cytokine Apo
29	58.4	2.7	1042	20	X86987	Human Apo-2 ligand
30	58.4	2.7	1042	21	A07425	Human Apo-2 ligand
31	58.4	2.7	1060	19	V15295	Human AGP-1 encodi
32	58.4	2.7	1521	18	T72851	Truncated apoptosi
33	58.4	2.7	1521	19	V29519	Human TRAIL deleti
34	58.4	2.7	1643	18	T85210	cDNA encoding huma
35	58.4	2.7	1751	18	T72847	Human apoptosis in
36	58.4	2.7	1751	19	V29518	Human TRAIL polype
37	58.4	2.7	1769	19	V63096	Human TL2 cDNA. H
38	54.8	2.5	774	21	299985	Primer used to amp
39	54	2.5	1366	18	T72848	Mouse apoptosis in
40	54	2.5	1366	19	V29520	Murine TRAIL polyp
41	54	2.5	3048	19	V15294	Murine AGP-1 encod
42	52.8	2.4	876	19	V42206	TNF-related apopto
43	51.4	2.3	8220	16	Q83529	P. falciparum Proj
44	51.4	2.3	8220	18	T72897	Plasmodium Proj3 g
45	51.4	2.3	8220	21	Z98286	P. falciparum Proj

ALIGNMENTS

RESULT 1	
ID V41489 standard; cDNA; 2191 BP.	
XX V41489;	
AC V41489;	
DT 24-SEP-1998 (first entry)	
XX Nucleotide sequence of mouse 499E9 gene.	

XX Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis; antagonist; autoimmune disorder; rheumatoid arthritis;	
KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;	
KW acute inflammatory response; antibody; antigen; cancer; ss.	
XX Mus sp.	

XX Key	Location/Qualifiers
FT CDS	125..1072
FT	/*tag= a
FT	/product= "mouse 499E9 protein"

XX WO9825958-A2.

XX 18-JUN-1998.

XX 12-DEC-1997; 97WO-US22766.

XX 13-DEC-1996; 96US-0032846.

XX (SCHE) SCHERING CORP.

XX Gorman DM, Mattson JD;

XX WPI; 1998-348452/30.

DR P-PSDB; W59654.

Mouse cell surface antigen, 499E9 protein - used to treat conditions associated with abnormal physiology or development

associated with abnormal physiology or development

Claim 4; Pages 8-11; 59pp; English.

This is the nucleotide sequence encoding the mouse 499E9 protein, used in the method of the invention to treat conditions associated with abnormal physiology or development. The 499E9 protein is expressed highly on polarised th1 T cells, binding of 499E9 to its receptor may result in either immune cell expansion or apoptosis. Antagonists of 499E9 may be used to modulate immune responses in abnormal situations, e.g. autoimmune disorders including rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as acute inflammatory responses in which T-cell expansion, activation or immunological T-cell memory play an important role. The antibodies can be used to raise anti-idiotypic antibodies which will be useful in detecting or diagnosing various immunological conditions related to the expression of antigens of 499E9. The antibodies, and fragments of 499E9 can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation (e.g. cancerous conditions) or degenerative conditions.

Sequence 2191 BP; 605 A; 461 C; 518 G; 607 T; 0 other;

```
Query Match      100.0%; Score 2191; DB 19; Length 2191;
Best Local Similarity 100.0%; Pval. No. 0;
Matches 2191; Conservative 0; Mismatches 0; Indels 0;
```

[illegible]

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Db	1741	gctaagggggcagaatact	gtttctggtgaccacatg	tagttattcttcttattct	ttttttt	1800
QY	1801	AACCTTAATAGAGCTCT	TCAGACTTGTCAAACTAT	GCAAGCAAAATAAATAA	AAAAATA	1860
Db	1801	aactttaaagagctctcag	actctgcaaaactatgcaag	caaaaataaaataaaata	aaaaata	1860
QY	1861	AAATGAATATCTTGAA	TAAATAGTAGGATGTTGG	TCCACGAGTGCCCTTCA	AAATTTAGAA	1920
Db	1861	aaatgaatatcttgaata	aagtaggaatgttggccac	caggtgcccttcaaat	tttagaa	1920
QY	1921	GCTAATTGACCTTTAG	GAGCTGACATAGCCAAA	AAGGATACATAATAGG	CTACTGAAAATC	1980
Db	1921	gctaattgactcttaggag	ctgacatagccaaaaggat	acataaataaggtactg	aaaaatc	1980
QY	1981	TGTCAGGAGTATTTAT	GCAATTTATTGAACAGG	TGTCCTTTTTTACAAAG	AGGTACACAAATG	2040
Db	1981	tgcagggagatcttagca	aatctatgcaacaggtgtc	ctttttttacaaagagct	acacaattg	2040
QY	2041	TAAATTTGTTTCTTTT	TTTTTTTCCCATAGAAA	TATGTACTATAGTTTAT	TCAGCCAAAAAACA	2100
Db	2041	taaatgttctctttttt	ttttcccatagaaaaatg	tactatagttatcagcc	aaaaaaca	2100
QY	2101	ATCCACTTTTTTAATT	TAGTGAAGTTATTTATT	TATCTGTACATAAATAA	AGCATCTTTT	2160
Db	2101	atccacttttaatttag	gaagttattttattatact	gtacataaataaagcat	gttttc	2160
QY	2161	TCAATGGCATTTT	TGGTACTTAAAAATG	CGC	2191	
Db	2161	tgaatggcatTTTTT	gggtacttaaaaatggc	2191		
RESULT	2					
V70284						
ID	V70284	standard; DNA: 2295 BP.				
XX	V70284;					
AC						
XX						
DT	11-FEB-1999	(first entry)				
XX						
DE	Human osteoprotegerin binding protein encoding DNA from the 32D-F3 ins					
XX						
KW	Human; osteoprotegerin binding protein; OPG binding protein; arthritis					
KW	osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;					
KW	hypercalcaemia; osteoclast differentiation and activation receptor;					
KW	Payet's disease; ss.					
OS	Homo sapiens.					
XX						
Key	Location/Qualifiers					
FH	158...1108					
FT	CDS					
FT	/**tag= a					
FT	/product= "osteoprotegerin binding protein"					
XX						
PN	WO9846751-A1.					
XX						
XX	22-OCT-1998.					
PF						
XX	15-APR-1998; 98WO-US07584.					
PR						
XX	30-MAR-1998; 98US-0052521.					
PR	16-APR-1997; 97US-0842842.					
PR	23-JUN-1997; 97US-0860855.					
XX						
PA	(AMGE-) AMGEN INC.					
XX						
PI	Boyle WJ;					
XX						
DR	WPI; 1998-594578/50.					
XX	P-PSDB; W83194.					
XX						

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 XX
 PS
 XX
 PS
 XX Claim 1; Fig 1; 47pp; English.
 XX
 CC The present sequence encodes human osteoprotegerin (OPG) binding protein
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 XX
 XX Sequence 2295 BP; 648 A; 487 C; 538 G; 622 T; 0 other;
 SQ

Query Match	97.9%	Score 2144.8	DB 19	Length 2295;
Best Local Similarity	99.4%	Pred. No. 0;		
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QY	1	GCCAGGACCTCTGTGAACCGTTCGGGGGGGGGGCGCGCTTGGCCGGAGTCTGCTCGCGGG	60	
Db				
QY	34	gccaggacctctgTgaaccgggtcggggcgggggcgccgtgcccggagctcgtcgtcgggcg	93	
Db				
QY	61	TGGGTGGCCGAGGGAAGGAGAGAACGATTCGGCGGAGCAGGGCGCCGAACTCCGGCGCGCG	120	
Db				
QY	94	tgggtggccggagggagagaacgatactcgcgagcaggcgcccgaaactccggcgccg	153	
Db				
QY	121	GGCCATCGCGGGCGCCAGCCGAGACTACGGCAAGTACCTGGCGACCTCGGAGGAGATGGG	180	
Db				
QY	154	cgccatcgccggcccgccagccagactacggaagtaacctgcgacgtcgaggagagatggg	213	
Db				
QY	181	CAGCGGGCCCCGGCTCCACACAGAGGGTCCGCTGCAACCGCGCGCTTGTGACCGGGTCC	240	
Db				
QY	214	cagcgccccggcgtccacacagaggctccgctgcaccgcgcctctctgcacggatcc	273	
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QY	241	GGCGCGGCACCGCGCGGGCTCCGCTCCATGTTCTGTGCGCTCTCTGGGGCTGGGACTGGG	300	
Db				
QY	274	ggcgccgccaaccggcgccctccgctccatgtctctggccctctctggggtgggactggg	333	
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QY	301	CCAGGTGCTGTGCAGCATCGCTCTGTCTCTACTTCTGCAGCGCAGATGGATCCTTAACAG	360	
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QY	334	ccagggtggctgcgagcatcgctctgttctctgtaaccttcgagcgcgagaTggatcccaacag	393	
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QY	361	AATATCAGAAGACAGCACTCACTCTCTTTATAGAACTCTGAGACTCCATGAAACGCAGG	420	
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QY	394	aatatcagaagacagcactcactgtctttatagaactcgtagactccatgaaaacgcagg	453	
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QY	421	TTTGCAGGACTCGACTCTGGAGAGTGAGACACACTACTCTACTCTCTGCAGGAGGATGAA	480	
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QY	454	tttgcaggactcgactctggagtggaagacacactactgactcctgcaggagatgaa	513	
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QY	481	ACAAAGCCTTTTCAGGGGGCCGTGCAGAGGAAGTGCACACATTTGTGGGGCCACAGCGCTT	540	
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QY	514	acaagcctttcaggggggccgtgcagaaggaaactgcacaacattgtggggccacagcgctt	573	
Db				
QY	541	CTCAGGAGTCCAGCTATGATGGGAAGGCTCATGTTGGATGTGGCCCAAGCGCAAGCC	600	
Db				
QY	574	ctcaggagctccagctatgaTggaaagctcatggTtggatgtggcccgagggcaagcc	633	
Db				

QY 601 TGAGGCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCA 660
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Db 634 tgaggccagccatttgcacacctccacc.tcaatgctgcgcagcatcccatcggttccca 693
QY 661 TAAAGTCACCTCTGCCCTTTGGTACCACUATCGAGGCTGGGCCAAGATCTCTAACATGAC 720
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Db 694 taaagtcactctgctctcttggTaccac; atcgaggctgggccaagatctctaacaatgac 753
QY 721 GTTAAAGCAACGGAAACTAAGGGTTAACTAAGATGGCTTTATTTACCTGTACGCCAACAT 780
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Db 754 gttaaagcaacggaactaagggttaac; aagatggcttctattacctgtacgccaacat 813
QY 781 TTGCTTTGGCATCATGAACATCGGGATCGGTACCTACCTACAGACTATCTTACGCTGATGGT 840
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Db 814 ttgctttcggca tca tgaaca tgggga; gcgtacctacagactatcttcagctgagt 873
QY 841 GTATGCTGTTTAAACACGAGCATCAAAATCTCAAGTTCTTCATTAACCTGATGAAGGAGGGAG 900
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Db 874 gtagtgcgttaaacaccagcatcaaaatc; caagtctctcataaactgatgaaaggaggag 933
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QY 1141 ATGCTATACATGTTAAGACTACTAAGTACATGCGCCACGGGTATGAAACTCAGC 1200
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QY 1201 CPTCTCTGTAGCCCTGTACAGGTTGTGATATGTAAGTCCATAGTGATGTAGATTTC 1260
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QY 1321 GGGAGAGGTATTCGGATGCTTATGAAAACTTACAGTGAAGCTATGGAAGGGGTACAG 1380
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Db 1353 gggagagggtattccgatgcttatagaaaaacttacagtgagctatggaagggggtcacag 1412
QY 1381 TCTCTGGGTCTAACCCCTGGACATGTCCTACTGAGAACCTTGAAATTAAGAAATGCCAT 1440
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Db 1473 gtcattgcaaaagaaa tga tagtgcgaagggttaagtctcttctgaaattgtcacattcgct 1532
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QY 1801 AACTTAATAGAGTCTTTCAGACTTGTCAAAACTATGCAAGCAAAATAATAATAAAAAATA 1860
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Db 1833 aacttaataagagcttcagactgtcaaaaactatgcaagcaaaa taaataaaataaaaaa 1892
QY 1861 AACTGAATATCTTCAATAAATAAGTAGGATGTTGTCACACAGTGCTTTCAAATTTAGAA 1920
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Db 1893 aaatgaataaccttgaaataaataagtaggagtgttggTccaccagggtcctttcaaattagaa 1952
QY 1921 GCTAATTTGACTTTTAGGAGCTGACATAGCCAAAAAGGATACATAATAGGCTACTGAAATC 1980
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Db 1953 gctaattgacttttggagctgacatagccaaaaaggatacacataataggctactg-aaatc 2011
QY 1981 TGTCAAGGAGTATTTATGCAATTTATTGAACAGGTGCTTTTTTTACAAGAGCTACAAATG 2040
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Db 2132 atccactttttaaatttagtgaagttattttattatctgtacaataaaagcattgtctc 2191
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Db 2192 tgaatgtaattttttgtgtacaaaaaat 2219
RESULT 3
299966
ID 299966 standard; DNA; 2299 BP.
XX 299966;
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA encoding a murine osteoprotegerin ligand (OPGL).
XX
KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
tumour necrosis factor receptor; type II transmembrane protein;
osteoclast differentiation; CSF-1; osteoclast activator;
immune response; osteoporosis; bone resorption; ss.
XX
OS Mus musculus.
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FH Key Location/Qualifiers
FT CDS 170..1120
FT /*tag= a
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PN W0200015807-A1.
XX
PD 23-MAR-2000.
XX
PF 13-SEP-1999; 99WO-DK00481.
XX
PR 15-SEP-1998; 98DK-0001164.
PR 02-OCT-1998; 98US-0102896.
XX
PA (MEBI-) M & E BIOTECH AS.
XX
PI Halkier T, Haaning J;
XX
DR WPI; 2000-271444/23.
DR P-PSDB; Y84419.

In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
to treat, prevent and ameliorate osteoporosis -
Disclosure; Page 82-85; 110pp; English.

The present sequence encodes a murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.

Sequence 2299 BP; 641 A; 494 C; 541 G; 623 T; 0 other;

Query Match 97.9%; Score 2144.8; DB 21; Length 2299;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2174; Conservative 0; Mismatches 12; Indels 2; Gaps

QY 1 GCACGAGACCCTGTGAACCGTTCGGGGCCGCCCTTGCCGGGAGTCCTCGCGGG 60
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 TGSGTGCCGAGAAGGAGAACATCGCGAGCAGGC GCCCAACTCTCGCGGCGCG 120
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 106 tggtgcccagaaaggagaacatcgagcagggccgcgaactcggcgccg 165
QY 121 CGCATCGCCGGCCAGCGAGACTACGGCAAGTACTTGGCGAGCTCGGAGGAGATGG 180
DB cgcatcgccccgccgagactacggcaagtacctgcagctcgagagagatggg 225
QY 181 CAGCGCCCCGGCTCCCACACAGAGGTCGGTGACCCCGCGCTTCGTGCACCGCTCC 240
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 226 cagcggccccggcgccccacagagggttcgctgcaccgcgcgttctgcaccggctcc 285
QY 241 GGCGCCGCCACCCGCGCTCCCGCTCCATTTCTTGGCCCTCTGGGCTGGGACTGGG 300
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 286 ggccgcaccaaccgcgcctccgatcttccttgccccctcctggcgctggactggg 345
QY 301 CCAGTGGTTCGAGCATGCTCTGTTTCTGTACTTTTCGAGCGCAGATGGATTCTTAACAG 360
DB ccaggtggtctgcagcatgctctgttctgtactttcgagcgagatgataccataaacg 405
QY 361 AAATACAGACAGCACNCTCACTGCTTTTATAGAACTCTGAGACNCTCATGAAGACGACGG 420
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 406 aatatcagaagacgactcaactgcgtcttatagaaatccctgagactccaatgaacaacgacg 465
QY 421 TTTCAGGACTCTGACTCTGAGAGTGAAGACACACTACCTGACTCTCTGAGCAGGATGAA 480
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 466 ttgtcaggactcgactctggagagtgaaagacacactaacctgactcctcaggagagatgaa 525
QY 481 ACAAGCCTTTTCAGGGGCCCTGCAGAAGAACTTGCAACACATTTGTGGGCCACACGCGTT 540
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 526 acaagccttlcaaagggcgctgcagaaggactgcacaacatttgtggggccacacgctt 585
QY 541 CTGAGGAGCTCCAGCTATGATGAAGGCTCATGTTGGATGTGGCCACCGAGGCAAGCC 600
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 586 ctcaaggactccagctatgatggaaggctcatagtgttgatgtggccagcgaggcaagcc 645
QY 601 TGAGGCCACGCCATTGSCACCTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCA 660
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 646 tgaagcccaagccatttgcacactcaccaalcaaatgctgcagcaatcccaatcgggtccca 705
QY 661 TAAAGTCACCTCTCTCTTTGGTACCACGATCGAGGCTGGGCGAAGATCTCTTAACATGAC 720


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QY 781 TTGCTTTTCGCATCATGAAACATCGGGAAGCTACCTACAGACTATCTTCAGCTGATGGT 840
Db 798 tgccttttcggca tca tgaacac tcyggaagcgtaccacagactatcttcagctgaaggt 857
QY 841 GTATGCTGTTAAACACGACATCAAAATCCCAAGTTCTCAATAACCTGATGAAGAGGGAG 900
Db 858 gtatgctgttaaaacacgacatcaaaatcccaagttctcataaacctgatgaagagaggaq 917
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QY 1021 TCCGGATCAAGATCGCAGCTACTTTGGGGCTTTCAAAAGTTTCAGGACATAGACTGAGACTC 1080
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QY 1081 ATTTCTGTGAACATTAGCATGGATGCTCTAGATGTTTGGAAACTTCTTAAAAATGGGATG 1140
Db 1098 attctgtggaacattagcatggatgctctagatgtttggaacctcttaaaaaatggatg 1157
QY 1141 ATGCTCTACATGTGAAGACTACTTAAGACACATGGCCACGCGTGTATGAACATCACAGC 1200
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QY 1380 GTCTCTGGGTCTAACCCCTGGACATGGCCACTGAGAACCTTGAATTAAGAAGATGCCA 1439
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Db 1456 tgcattgcatagaaatgatagtgtgaagggttaagttcttttgaaattgttacattgcgc 1515
QY 1500 TGGGACCTGCAAAATAGTCTCTTTTCTTAATGAGGAGAGAAAATATATGATTTTAT 1559
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Db 1574 ataagtctaaagtataatttcagggtgaatgtttctgtgcaagttttgtaaattata 1633
QY 1620 TTTGTGCTATAGTATTGATTCAAAATATTTAAAAATGCTCACTGTTGCATATTTAAAT 1679
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Db 1754 agctaaggggcgagaactctgttctgtgtgaccacatgtagttctattcttcttcttt 1813
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QY 1860 AAAATGAATATCTTGAATAATAAGTAGGATGTTGGTCACCAGGTGCCTTTTCAAAATTTAGA 1919
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Db 1874 aaaaatgaatacccttgaataaataagtaggtgttggccaccaggtgcctttccaattaga 1933
QY 1920 AGCTAATTCAGCTTTAGGAGCTGACATAGCCAAAGGATACATAATAGGCTACTGAAAAT 1979
Db 1934 agctaattgacttttaggagctgacatagccaaaagga-acataataggctactg-aaat 1991
QY 1980 CTGTCAGGAGTATTTATGCAATTTATGACAGGTGCTCTTTTTCACAGAGCTACAAAT 2039
Db 1992 ctgtcagagattattatgcaattattgaaacaggtgctttttttacaagagctacaaaat 2051
QY 2040 GTAAATTTT-GPTTCTTTTTCATAGCAATGACAAATCTACTATATGTTTATCAGCCAAAAA 2098
Db 2052 gtaaatcttggctctctcttctcccatagaaaatgactatagtttacagccaaaaa 2111
QY 2099 CAATCCACTTTTAAATTTAGTGAAGTTATTTTATTTATCTGTACATAAAGCAATTTGTT 2158
Db 2112 caatccacttttaatttagtgaagttattttattattactgtacataaaaagcattgct 2171
QY 2159 TCTGAATGGCATTTTGGTACTTAAAAAT 2188
Db 2172 tctgaatgttaatttttggtaaaaaaat 2201

RESULT 5
V41377 ID V41377 standard; cdna; 1630 BP.
AC V41377;
XX
DT 08-OCT-1998 (first entry)
XX
DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
XX
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 3..887
FT /*tag= a
FT /product= "murine RANKL (ligand for RANK)"
XX
PN WO9828426-A2.
XX
PD 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US23775.
PF
PR 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Anderson DM, Galibert LJ, Maraskovsky E;
XX
DR WPI; 1998-377657/32.
DR P-PSDB; W69956.
XX
PT New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells
XX
PS Claim 25; Pages 55-57; 80pp; English.
XX
CC This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
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RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF- κ B by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used as adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF- α . The products can also be used for detection and drug screening.

xx
SQ Sequence 1630 BP; 436 A; 355 C; 319 G; 460 T; 0 other;

Query Match 73.7%; Score: 1615.8; DB 19; Length 1630;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 189 CCGCGCTCCACAGCGGTCCTGCAACCGCGCTCTCTGACCGGCTCCGCGCGCGC 248
DB 1 CCGCGCTCCACAGCGGTCCTGCAACCGCGCTCTCTGACCGGCTCCGCGCGCGC 60
QY 249 CACCGCGCGCTCCGCTCCATGTTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 308
DB 61 CACCGCGCGCTCCGCTCCATGTTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 309 TCTGACGATCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 368
DB 121 TCTGACGATCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 369 AACACAGCACTCACTGTTTATAGAAATCTGAGACTCCATGAAACGCGAGTTTGCAGG 428
DB 181 AAGACGACGCTCACTGTTTATAGAAATCTGAGACTCCATGAAACGCGAGTTTGCAGG 240
QY 429 ACTCGACTCTGGAGTGAAGACACACTCTCTGACTCTCTGACGAGGATCAACAGCCCT 488
DB 241 ACTCGACTCTGGAGTGAAGACACACTCTCTGACTCTCTGACGAGGATCAACAGCCCT 300
QY 489 TTCAGGGGGCGCTGCAGAAAGAACTGCAACACATTTGTGGGGCCACACGCGTCTCTCAGGAG 548
DB 301 TTCAGGGGGCGCTGCAGAAAGAACTGCAACACATTTGTGGGGCCACACGCGTCTCTCAGGAG 360
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QY 609 AGCCATTGTCACACCTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCATAAAGTCA 668
DB 421 AGCCATTGTCACACCTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCATAAAGTCA 480
QY 669 CTCTGCTCTCTTGGTACCGAGTCGAGGCTGGGGCCAAAGATCTCTAACATCAGCTTAAGCA 728
DB 481 CTCTGCTCTCTTGGTACCGAGTCGAGGCTGGGGCCAAAGATCTCTAACATCAGCTTAAGCA 540
QY 729 ACGGAAACTAAGGGTTAACCAAGATGGCTTCATTATACCTGTACGCCAACATTTGCTTTC 788
DB 541 ACGGAAACTAAGGGTTAACCAAGATGGCTTCATTATACCTGTACGCCAACATTTGCTTTC 600
QY 789 GGCATCATGAACATCGGGNAGCGTACCTACACACTATCTCTACGCTGATGTTATGTCG 848
DB 601 GGCATCATGAACATCGGGNAGCGTACCTACACACTATCTCTACGCTGATGTTATGTCG 660
QY 849 TTAACACCGACATCAAAATCCCAAGTCTCATAACTGTGTAAGAGGAGGAGGACGACGAA 908
DB 661 TTAACACCGACATCAAAATCCCAAGTCTCATAACTGTGTAAGAGGAGGAGGACGACGAA 720
QY 909 ACTGGTGGGCAATTCGAATTCACACTTATTCCTCAATATTTGGGGGATTTTTCAGC 968
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DB 721 actggtgggcaattctgaattccactttttatccataaattgtgggggatttttcaagc 780
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DB 781 tccgagctgggagagaaattagcattcagggtccaaaccttccctgctggtgacccgagtc 840
QY 1029 AAGATGCGACGCTACTTTGGGGCTTTCAAGTTCAGGACATAGACATGAGACTCATTTTCG 1088
DB 841 aagatgagcgtactttgggcttttcaagttcaggacatagactagactcatttcgtg 900
QY 1089 GAACATTAGCATGATGCTCTAGATGTTGGAAACTTCTTAAAAATGCATGATCTAT 1148
DB 901 gaacattagcgtatgctcctagatgtttggaaacttcttaaaaaatgtagatgctctat 960
QY 1149 ACATGTGTAAAGACTACTAAGAGACATGCCACGCTGATGAAACTCACAGCCCTCTCTC 1208
DB 961 acatgtgtaagactactaagagacatggccacagggtgatgaaactcacagccctctctc 1020
QY 1209 TTGAGCCCTGTACAGGTTGTTGTTATATGTAAAGTTCATAGTGATGTAGATTTCATGCTGAT 1268
DB 1021 ttgagcctgtacaggtttgtatagttaaagtcctatagggttagatttcatggtgat 1080
QY 1269 TACACACGGTTTTACAAATTTTGTAAATGATTTCTTAAAGATTAACACAGATTGGGAGAGG 1328
DB 1081 tacacaacgggttttacaattttgtaattgtaatttcct-agaattgaaccagattggagaggg 1139
QY 1329 TATTCCGATGCTTATGAAAACTTACACGTGAGCTATGAAAGGGGTGACAGTCTCTGG 1388
DB 1140 tattccgagcttatgaaaaacttacacgtgagcgtatgaaagggttcacagtcctcctgg 1199
QY 1389 TCTAACCCCTGGACATGTGCCACTCAGAACCTTGAATTAAGAAATGCAATGCATGCTATGCT 1448
DB 1200 tctaaccctggacatgtgccactgagaaacctgaaattaaagagatgccatgctatgct 1259
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DB 1260 aaagaaatgtagtggaggggttaagttcttttgaattgttaacattgcgtcggagcctg 1319
QY 1509 CAATAAGTCTCTTTTCTTAATGAGGAGAGAAATAATATATGTTTATATATATGCT 1568
DB 1320 caataagttctcttttcttaattgaggagagaaaaatatagtattttataataatgct 1379
QY 1569 AAAGTTATATTTCAGTGTAAATGTTTCTGTGCAAAAGTTTGTAAATTTATTTTCTGCTA 1628
DB 1380 aaagtataattcagggtgataatgtttctgtgcaaaagttttgtaaatatatttctgcta 1439
QY 1629 TAGTATTGATTCAAAATATTAAATAATGCTCTACTGTGTGACATATTAAATGTTTAAAT 1688
DB 1440 tagtattgtatcctaaatatttataaaatgtctcactgttgacataatttaatttaaat 1499
QY 1689 GTACAGATGATTTAACTGGTGCACATTTGTAATTTCCCTGAGAGTACTCGTAGCTAAGGG 1748
DB 1500 gtacagatgattttaaactggtgcactttgttaattccctcgaagggtactcgtagctaaagg 1559
QY 1749 GGCAGATACGTTTCTGCTGACACACATGATGTTTATTTTCTTTTATTTTAACTTAAT 1808
DB 1560 ggcagataactggtttctcgttgagccacatgtagttttattcttcttcttttaactta 1619
QY 1809 AGAGTCTTCAG 1819
DB 1620 agagtcttcag 1630
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RESULT 6
V41371
ID V41371 standard; cDNA; 1630 BP.
XX
AC V41371;
XX
DT 08-OCT-1998 (first entry)
XX
DE NF- κ B receptor activator RANK ligand (RANKL) encoding cDNA.
XX

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.

OS Mus musculus.

FH Key Location/Qualifiers
 FT CDS 3..887

FT /*tag= a
 FT /product= "murine RANKL (ligand for RANK)"

PN WO9828424-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23866.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0813509.

XX (IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI; 1998-377655/32.

XX P-PSDB; W68292.

XX New isolated receptor activator of necrosis factor-kappa B - useful

XX for, e.g. developing products for regulating an immune or

XX inflammatory response, treating toxic shock or sepsis

XX Example 7; Pages 55-57; 80pp; English.

XX This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

Query Match 73.7%; Score 1615.8; DB 19; Length 1630;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1628; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 189 CCGGCGTCCACACAGAGGTCCGCTGCACCGCGCCCTCTCCACGGCTCCGGCGCGC 248

DB 1 ccg9cgtcccaacagag9gtccgctgcacccgcg9cctctctgcac9cgtccg9cgc9c 60

QY 249 CACCGCGCGCTCCCGCTCCATGTTCCCTGGCCCTCTGGGGTGGGACCTGGCCAGGTGG 308

DB 61 caccgcgcgtccgcctccatgttccctg9ccctcctggggtg9gactggccaggtg9 120

QY 309 TCTGAGCATCGTCTGTCTGTACTTTCGAGCGCAGATGGATCCTACAGAAATATCAG 368

DB 121 tctgcagcatcgctgtctgtctgtactctgagcgcagatggatcctaacaagaatcag 180

QY 369 AAGACGACACTCACCTGCTTTATAGAACTCCAGACTCCATGAAAACGACGTTTGCAGG 428

DB 181 aagacagcactcactgcttttatagaatcctgagactccatgaataacgcagatttcag9 240

QY 429 ACTCGACTCTGGAGAGTGAAGACACACACTACTGACTCTCTGCAGGAGGATGAACAGCCT 488
 DB 241 actcgactctggagagtgaagacacacactacactgactcctcctgaggagatgaacaagcct 300
 QY 489 TTCAGGGGGCGTGCAGAGAAGCAACTGCAACACATTTGTGGGCCACAGCGCTTCTCAGGAG 548
 DB 301 ttcagggggccgtgcagagaagaactgaacaacattgt9gg9ccacagc9cttctcagagag 360
 QY 549 CTCAGCTATGANGGAAGGCTCATGCTTGGATGTGGCCCGCCAGCGAGGAGCCTTGAGGCC 608
 DB 361 ctccagctatgatgaaggtcctggttggatgtg9cccgagcagcgaagcctgag9ccc 420
 QY 609 AGCCATTTGGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCATTAAGTCA 668
 DB 421 agccatttgcacacctcaccatcaatgctgcagcagcaccatcggttcccaataagtca 480
 QY 669 CTCTGCTCTCTTGGTACACGATCGAGCTGGGCCAAGACTCTTAACATGAGCTTAAGCA 728
 DB 481 ctctgctctcttggctaccagatcg9gctg9g9ccaaagatctctaacatgacgttcaagca 540
 QY 729 ACGGAAACTAAGGGTTAACCAGATGCTTCTATTACTCTGTACGCCCAACATTTGCTTTC 788
 DB 541 acggaaaactaa9ggttaaccagatggtctctattacctgtacgccaacatttgccttc 600
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 DB 601 ggcacatgaacatcg9gaagcgtacacacagactatcttcagctg9gtgtatgctg 660
 QY 849 TTAACACGACATCAAAATCCCAAGTTCTCATAACTGATGAAAGGAGGAGCAGCAAAA 908
 DB 661 ttaaacccagcatcaaaatcccaagttctcataaccctg9atgaaag9gag9gagcag9aaa 720
 QY 909 ACTGGTGGGGCAATTCGAATTTCCACTTTTATCCATAAATTTTGGGGGATTTTTCAGGC 968
 DB 721 actggctgggcaattctgaattcccacttttattccataaattgttgggggatttttcaagc 780
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 QY 1029 AAGATGGAGCTACTTTGGGGCTTTCAAAGTTTCAGGACATAGACATGACATTCATTCGTG 1088
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 DB 961 acatgtgtaagactactaaagagacatggccacg9gtgtatgaaactcacg9cctctctc 1020
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 QY 1329 TATTCCGATGCTTATGAAAACCTTACACGTGAGCTATGGAAGGGGGTCCACAGTCTCTGGG 1388
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 QY 1389 TCTAACCCCTGGACATGCTGCCACTGAGAACCTTGAATTTAAGAAATTAAGAAATGCCATGTC 1448
 DB 1200 tctaaaccttggacatgtgccactgagaaccttgaataatgaag9gatgccatg9t9t9t9t9 1259
 QY 1449 AAAGAAATGATGTGCAAGGGTTAAGTTCTTTTGAATTTTACATTTCCGCTGGGACCTG 1508
 DB 1260 aaagaaatg9at9t9gaag9gtt9aag9tctt9t9t9t9t9t9t9t9t9t9t9t9t9t9 1319
 QY 1509 CAAATAAGTTCTTTTTTCTTAATGAGGAGAAAAATATATGTTATTTATATATATGCT 1568

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Db 1320 caataaagttcttttttcttaataagagag;gaaataataatgatttttatacaatgtct 1379
QY 1569 AAAGTATATTTTCAGGTGTAATGTTTTCT;TGCAAGATTTTGTAAATTTATATTTGTGCTA 1628
|||||
Db 1380 aaagtattatttcaggtgtaattgtttct;tgcaaaagttttgtaaatatatttggcta 1439
QY 1629 TAGTATTTGATTCAAAATATTTAAAAATG;CTCACTGTTGACATATTTAAATGTTTAAAT 1688
|||||
Db 1440 tagtatttgattcaaaaattttaaaaatg;ctcaactgttgacataatttaagtctttaaat 1499
QY 1689 GTACAGATGTTATTTAACTGGTGCACCTTTG;AATTCCTCGAAGGTACTGTAAGG 1748
Db 1500 gtacagatgtatttaactgg;gcactttg;aattccctgaaggtactcgtagctaaagg 1559
QY 1749 GGCAGATPACTGTTTCTCGTGACACACATG;AGTTTATTTCTTTTATTTCTTTTAACTTAA 1808
|||||
Db 1560 ggcagaaacactgtttctgtgtgaccacatg;agtttattcttatttatttcttttaactta 1619
QY 1809 AGAGTCTTCAG 1819
|||||
Db 1620 agagtcttcag 1630
RESULT 7
V69886
ID V69886 standard; cDNA to mRNA; 1538 BP.
XX V69886;
AC
XX
XX 10-FEB-1999 (first entry)
DE Nucleic acid encoding an OCIF-binding molecule (OBM).
XX
XX Osteoclastogenesis inhibitory factor; OCIF: OCIF-binding molecule; OBM;
KW osteoclast; bone absorption factor bone disorder; calcium metabolism;
KW ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifier:
FH 125..1075
FT CDS /*tag= a
XX
XX W09846644-A1.
XX
XX 22-OCT-1998.
XX
XX 15-APR-1998; 98WO-JP01728.
XX
XX 02-DEC-1997; 97JP-0332241.
XX 15-APR-1997; 97JP-0097808.
XX 09-JUN-1997; 97JP-0151434.
XX 12-AUG-1997; 97JP-0217897.
XX 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW) SNOW BRAND MILK PROD CO LTD).
XX
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
XX WPI; 1998-594563/50.
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
PT for, e.g. treatment and investigation of disorders of bone and
PT calcium metabolism
PT
XX
XX Claim 9; Pages 108-109; 151pp; Japanese.
PS
XX The present sequence encodes an osteoclastogenesis inhibitory factor
CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC separation and maturation of osteoclasts in the presence of bone
CC

CC absorption factors such as calcitriol or parathyroid hormone (PTH).
CC OBM is isolated from stroma cells cultured in the presence of a bone
CC absorption factor by separation and solubilisation of membrane proteins
CC then affinity chromatography using OCIF. It exists in a full-sequence
CC form and a solubilised form (sOBM) which is a shorter chain. OBM may be
CC used for screening potential inhibitors and modifiers of its biological
CC activity, and screening for receptors to OBM which mediate its function.
CC These substances can then be used in the treatment of disorders of bone
CC function and calcium metabolism. The antibodies can be used for assay
CC of the protein, for investigative and diagnostic purposes, and as
XX components of drugs.
SQ Sequence 1538 BP; 382 A; 381 C; 416 G; 359 T; 0 other;

Query Match 69.6%; Score 1525.4; DB 19; Length 1538;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCAGGACCTCTGTGAACCGTCCGGGGCGGCGCCCTTGCCTGGCGGAGTCTGCTCGCGCG 60
Db 1 gccaggacctctgtgaaccggtccgggcccggggccctgcccgggagctctgtctcgcg 60

QY 61 TGGGTGGCGAGGAGGAGAGAACGATCGCGAGGAGGCGCGCCGAACTCCCGGGCGCCG 120
Db 61 tgggtggccgaggaaggagagacgatcgcgagcagggcgccgaactccggcgcg 120

QY 121 CGCCATGCCCGCGCGCGAGACTACGCGAAGTACCTTCGCGAGCTCGGAGGAGATGGG 180
Db 121 cgccatgcccgggcccagcgagactacggaagtacctgcgagctcgagagagatggg 180

QY 181 CAGCGGCCCGCGCTCCACACAGAGGTCCGCTGACCGCGCGCCCTTCTGCACCGCTCC 240
Db 181 cagcgcccgccgctcccaacagagggctcgctgcaaccgccccttctgcaacgctcc 240

QY 241 GCGCGCGCCACCGCGCGCTCCCGTCCATGTTCTGGCCCTCTCTGGGCTGGGACTGGG 300
Db 241 ggcgcgcgcccgcgcctccgctccatgttccctggccctctggggaactggg 300

QY 301 CCAGGTGGTCTGCAGCATCGCTCTGTCTGTACTTTCGAGCGCAGATGGATCCTAACAG 360
Db 301 ccaggtggtctgcagcatcgctctgtctgtacttctgagcgagatggatcctaaca 360

QY 361 AATATCAGAAGACAGCACTCACTGCTTTTATAGAATCTTGAGACTCCATGAAACGCGG 420
Db 361 aatatcagaagacagcaactcaactgcttttatagaaacctgagactccatgataaac 420

QY 421 TTTGCAGGACTCGACTCTCGAGAGTGAACACACACTACCTGACTCTCTGAGGAGGATGAA 480
Db 421 ttgagagactcgactctgagagtgaagacacactacactgactcctgagggagatgaa 480

QY 481 ACAAGCCTTTTCAGGGCGCGCTGCAGAAAGAACTGCAACACACTTGTGGGCGCACAGCGCTT 540
Db 481 acaagccttccaggggcccgtgcagaaggaactgcaaacacatgttggggcccagcgctt 540

QY 541 CTCAGGAGCTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCCCGCAGGCGCAAGCC 600
Db 541 ctccaggagctccagctatgattggaaggctcatggttgatgtgtgcccagcgagcaagcc 600

QY 601 TGAGGCGCCGACCATTTGACACACTCACCATCAATGCTGCCAGCATCCCATCGGGTCCCA 660
Db 601 tgagggccagccatttgcaacctcaccatcaatgtctgcagcatcccatcggggtccca 660

QY 661 TAAAGTCACTCTGTCTCTTGTGTACACGATCGAGGCTGGCGGCGCAAGATCTCTAACATGAC 720
Db 661 taaagtcaactctgtctctgtgtaccacgatcgaggtggtggcagaatctctaaatgac 720

QY 721 GTTAAGACACGGAACAACTAAGGTTAAACAAAGATGCGCTTCTATTACCTGTACCCCAACAT 780
Db 721 gttaaagcaacgaaacactaaagggttaacaaagatggcttctattacctgtcacgccaacat 780

QY 781 TTGCTTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGTT 840
|||||

XX 30-MAR-1998; 98US-0052521.
 PR 16-APR-1997; 97US-0842842.
 PR 23-JUN-1997; 97US-0880855.
 XX (AMGE-) AMGEN INC.
 XX Boyle WJ;
 PI
 XX WPI; 1998-594578/50.
 DR P-PSDB; W83195.
 XX
 PT Nucleic acid encoding osteoprotegerin binding protein - useful for
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 and for diagnosis
 XX
 PS Claim 1; Fig 4; 47pp; English.
 XX
 CC The present sequence encodes human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 XX
 SQ Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;

Query Match 51.18; Score 1118.8; DB 19; Length 2274;
 Best Local Similarity 76.3%; Pred. No. 3.7e-253;
 Matches 1659; Conservative 0; Mismatches 437; Indels 78; Gaps 20;

XX	30-MAR-1998; 98US-0052521.	QY	454	-----ACTACCTGACTCCTCGAGGAGGATGAACAAGCCCTTTTCAGGGGCGCGTGAGAA	507
PR	16-APR-1997; 97US-0842842.	Db	511		570
PR	23-JUN-1997; 97US-0880855.			aaattaaatcaccgtgattcattgtaggaataaaacaggcccttcaadggagctgcaaaa	
XX	(AMGE-) AMGEN INC.	QY	508	GGAACCTGCAACACATTTGTGGGGCCACACGCGCTTCTCAGGAGCTCCAGCTATGATGGAGG	567
XX	Boyle WJ;	Db	571		630
XX				gaattacaacatatcgttgatcacagacatcacagacagagaaagcagatggtggtatg	
QY	WPI; 1998-594578/50.	QY	568	CTCATGTTGGATGTGGCCCGCAGCGCAAGCCCTGAGGCCCGCCAGCCATTTTGCACACCTGAC	627
DR	P-PSDB; W83195.	Db	631		690
XX				ctcatggttagatctgccaagagagcaagcttgaagctcagcctttgtctcatctc	
PT	Nucleic acid encoding osteoprotegerin binding protein - useful for	QY	628	CATCAATGCTGCCAGCATCCATCGGCTTCCATAAAGTCACTCTGCTCTTCTTGTGTACCA	687
PT	e.g. treating bone diseases by modulating osteoclast differentiation	Db	691		750
XX	and for diagnosis			tattaatgccacgacatcccatctggttcccaataaagtgatgtctctcttgggtacca	
XX		QY	688	CGATCGAGGCTGGCCCAAGATCTTAACATGACGTTAAGCAACGAAACCTAAAGGTTTAA	747
XX	Claim 1; Fig 4; 47pp; English.	Db	751		810
CC	The present sequence encodes human osteoprotegerin (OPG) binding protein.			tgatcggggttgcccaagatctccaacatgacttttagcaatggaaaactaatagttaa	
CC	Host cells transfected with vectors containing nucleic acid molecules	QY	748	CCAAGATGGCTTCTATTACCTGTACGCCCAACATTTGCTTCCGGCATCATGAACATCGG	807
CC	encoding OPG binding protein are used to produce recombinant OPG binding	Db	811		870
CC	protein. OPG binding protein is used in binding assays to determine			tcaggatggctttattacactgtatgcacacatttggcttccgacatcatgaaacttcagg	
CC	osteoprotegerin (OG) in biological samples; to screen for specific	QY	808	AAGCGTACCTACAGACTATCTTCAGCTGATGGTGTATGTCTGTTAAACCAACATCAAAAT	867
CC	binding agents (particularly agonists and antagonists, including	Db	871		930
CC	intracellular proteins); to raise Ab (useful in immunoassays for			agacctagctacagatctctcaactaatgggtcactcaataaacacacagcatcaaat	
CC	detection of OPG binding protein) and to identify compounds that	QY	868	CCCAAGTTCCTCATACCTGATGAAGGAGGAGGAGCACCAGAAACCTGGTCGGCAATTCTGA	927
CC	modulate binding of OPG binding protein to osteoclast differentiation	Db	931		990
CC	and activation receptor (ODAR). The nucleic acid molecule encoding OPG			cccaagtctctacacctgatgaaagaggaagcaccaaagtattggtcagggaaattctga	
CC	binding protein can be used to detect OPG binding protein-encoding	QY	928	ATTTCCACTTTTATTCATAAATGTTGGGGGATTTTCAAGCTCCGAGTGTGTAAGAAT	987
CC	sequences, e.g. screening for related sequences, also to produce	Db	991		1050
CC	transgenic animal models, while complementary sequences are used for			attccattttttccataaacagtgggagatttttaagttagctgctgagaggaaat	
CC	antisense regulation of OPG binding protein expression. Modulators of	QY	988	TAGATTTACGGTGTCCAAACCTTCCCTGCTGGATGCCGGATCAAGATGGAGCGTACTTTGG	1047
CC	OPG binding protein, particularly soluble forms of OPG binding protein	Db	1051		1110
CC	or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,			cagcatcgaggtctccaaacctcttactggtaccggtcaggtgcaacatacttgg	
CC	bone loss caused by arthritis or metastases, hypercalcaemia, Paget's	QY	1048	GGCTTTCAAAAGTTCAAGACATAGACTGAGACTCATTTTCGTGGAACATTAGCATGATGTC	1107
CC	disease, periodontal disease, osteoporosis, loosening of prostheses,	Db	1111		1167
CC	optionally in combination with agents that promote bone growth.			ggcttttaaagtcgagatagattgagccccagtttttggagtggtt---atglatcttc	
XX		QY	1108	CTAGATGTTTTGGAAACTTCTTAAAAA-----ATGGATGATGCTATACATGTGTAAGA	1160
XX	Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;	Db	1168		1227
				ctgagatgttggaaacattttttaaacaagcccaagaaagatgtatatagtggtgaga	
		QY	1161	CTACTAGAGACATGCGCCCGGGTGTATGAACCTCAGAGCCCTCTCTTGTAGCCTGTAC	1220
		Db	1228		1287
				ctactaagagggcatggccccaaaggtacacgactcagtatccatgctcttgacctgtag	
		QY	1221	AGGTTGTTGTTATGTAAGTCCATAGGTGATGTTAGATTTCATGTTG-ATTACACACCGT	1279
		Db	1288		1347
				agaaacacgclatttacagccagtgggagatggttagactcatggtgtgtttacaaatggt	
		QY	1280	TTTACAAATTTTGAATTCCTTAAAGATTTGAACCTGAAACCTGGAGAGGATTTCCGATGC	1339
		Db	1348		1406
				ttttaaattttgtaataatcct-agaattaaacagattggagcaattacgggttgac	
		QY	1340	TTATGAAAACCTTACAGCTGAGCTATGAAGGGGGTGCACGCTCTGTGGGTCTAACCCCTG	1399
		Db	1407		1450
				ctlatgagaacagcatgtgggctatggggggg-----ttggctccctg	
		QY	1400	GACATGTCGCACTCAGAACCTTGAATTAAGAAGATGCCATGTCATTTCGAAAGAAATGAT	1459
		Db	1451		1508
				gtcatgtgcccttcgcagct-gaagtggagaggggtgctcatct-agecgaattgaagat	
		QY	1460	AGTGTGAAGGGTAAAGTCTTTTGAATTTGTTACATTTGGCTGGGACCTGCGAAATAAGTTC	1519
		Db	1509		1567
				catctgaaaggggcaaatctcttttgaaattgttaccacatgctggaaacctgcgaaaaaac-	
		QY	1520	TTTTTTTCTAATGAGGAGAGAGAAAAATATATGTTATTTTATATGTTCTAAAGTTATAT	1579

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Db 1568 --tttttcaatgaggagag-aaataca/gtatctttcatacaatcataagttatat 1624
Qy 1580 TCAGGTGTAATGTTTCTGTCGCAAGTGTTCGTAATTAATTTATTTGTCGTATAGTATTTGAT 1639
Db 1625 tcagatgtaatgtttcttcttgcaagatagtaataattatattgtgctatagttatgat 1684
Qy 1640 TCAAAATATTTAAATGTCACACTGTTG/CATATTTAAATGTTTAAATGTACAGATGTA 1699
Db 1685 tcaaaatatttaaaaatgtcttgctgttg/cataatttaattgttttaaatgacagacata 1744
Qy 1700 TTTTAACGTGGTCACTTTGTAATCCCTGTG- ----AAGGTACTGCTAGTAAAGGGGGCAGA 1754
Db 1745 tttaactggtgcactttgtataatccctgt/ggaaacttcagctaaaggagggaataaaa 1804
Qy 1755 ATACTGTTCTTGGTGACACATGTAGTATT/TCTCTTATTTCTTTTAACCTTAATAGA-GT 1813
Db 1805 atgtgtttcttaataatacaaatgcagatat; tttctgttcttttaagttaaatagattt 1864
Qy 1814 CTTTCAGACTTTGTCAAACTATGCAAGCA/ATAAATAAATAAATAAATAAATAAATAATCTT 1873
Db 1865 tttcagacttgcagactgtgc-----aaataatlaaatggatgcctt 1910
Qy 1874 GAATAATAAGTAGGATGTGTCACCAAGG/GCCTTTCAAAATTTAGAACTAATTCACATTT 1933
Db 1911 gaaataaagcagatgtgtgcccacag/gcctttcaaatattagaactaattgaactt 1970
Qy 1934 AG-CAGCTGACATAGCCAAAAGGATACAAATAGGCTACTGAAAATCTGCAGAGTAT 1992
Db 1971 agaagctgacatgccaataagatacataaataaggccactg-aaatctgtcaagagcag 2029
Qy 1993 TTATGCAATTTATTCACAGGTGCTTTT/TTCACAGAGCTACAAATTTGTAATTTGTTT 2052
Db 2030 ttataaatgttgacaggtg--tttttcacaaagtgcgcaaatgtaccttt----- 2082
Qy 2053 CTTTTTTTCCCATAGAAAATGTACTATATTTATGCCCCAAAACAAATCCACTTTTATA 2112
Db 2083 -tttttttttccaaatagaaaagtatt;gtggtttatcagcaaaaagtcocatttta 2141
Qy 2113 ATTTAGTGAAGTATTATTATTATCTGTC/CAATAAAGCATTTCTTCTGATGCAATTT 2172
Db 2142 atttagtaaatgtta---tcttactgt;caataaaacattgccttctgaatgttaatt 2198
Qy 2173 TTTTGGTACTTTAAAA 2186
Db 2199 ttttggtaaaaaa 2212

RESULT 10
X80223
ID X80223 standard; cDNA; 1823 BP.
XX
AC X80223;
XX
DT 17-AUG-1999 (first entry)
XX
DE Human TRANCE encoding cDNA.
XX
KW TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
KW TNF-related activation induced cytokine; immune response; cancer;
KW autoimmune disease; HIV; hypersensitivity; allergen; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..738
FT /*tag= a
XX
XX WO9929865-A2.
XX
PN 17-JUN-1999.
XX
PD 14-DEC-1998; 98WO-US26486.
XX
PF
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XX 11-DEC-1998; 98US-0989479.
PR 12-DEC-1997; 97US-0989479.
PR 03-MAR-1998; 98US-0034099.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI Choi Y, Josien R, Steinman R, Won B;
XX WPI; 1999-385609/32.
DR P-PSDB; Y17873.
XX
XX TNF like proteins for treating autoimmunity and cancer
XX Claim 1; Fig 1; 164pp; English.
XX
XX The present sequence encodes human TNF-related activation induced
XX cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX variants, fragments, derivatives or analogues may be used as modulators
XX of immune response in a mammal comprising, antisense sequences to
XX TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX Agonists and antagonists of TRANCE, can be used to modulate immune
XX response by increasing or decreasing the life span of mature dendritic
XX cells and increasing or decreasing T cell activation. These techniques
XX are especially useful for treating immune system related conditions such
XX as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
XX The TRANCE polypeptides can be used to increase the viability of
XX dendritic cells in vivo or in vitro, especially when used in conjunction
XX with proteins of the tumour necrosis factor (TNF) superfamily (especially
XX CD40L or TNF-alpha).
XX
XX Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;
XX
XX Query Match 43.7%; Score 957.2; DB 20: Length 1823;
XX Best Local Similarity 77.0%; Pred. No. 2.8e-215;
XX Matches 1433; Conservative 0; Mismatches 358; Indels 71; Gaps 19;
Qy 344 CAGATGGATCTTAACAGATATATCAGAAGACAGCACTACTGCTTTTATAGATCTCGAGA 403
Db 1 cagatggatcttaalagaataatcagaagatggcactcactgcatttatagaatttga 60
Qy 404 CTCCTGAAAACGCGAGTTTGCAGGACTCGACTCTGGAGAGTGAAGACAC- ----ACTA 457
Db 61 ctccatgaaaatgcagattttcaagacacactctggagagtcagatatacaataaata 120
Qy 458 CCTGACTCTCGAGGAGGATGAACAAGCCTTTCAGGGGCGCTGCAGAGGAGCACTGCA 517
Db 121 cctgattcatgtaggagaataaacaaggcctttcaaggagctgtgcaaaagaaataca 180
Qy 518 CACATTGTGGGCCACAGCGCTTCTCAGGAGCTCCAGAGCTATGATGAGGAGCTCATGGTTG 577
Db 181 catatcgttggatcacagcacatcagagcagagaaagcagatggtgagtgctcatggtta 240
Qy 578 GATGTGGCCCGAGGAGCAAGCCTGAGGCCCGCCATTTGCACCTCCACCATCAATGCT 637
Db 241 gatctggcagaagagagcaagcttgaaagctcagcctttgtctcactcactataatg 300
Qy 638 GCCAGCTCCCATCGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACACGATCGAGCG 697
Db 301 accgacatcccatctggttccataaagtgatgtctctctgtgtaccatgatcggggg 360
Qy 698 TGGGCAAGATCTCTAACATGACGTTAAGCAACGAGAAAATAAGGTTTAAACAAGATGGC 757
Db 361 tggggaagatctccaacatgacttttagcaatggaactaatagtttaacagagatg 420
Qy 758 TTCATTACCTGTACGCCAACATTTGCTTTCGGCATCATGAACATCGGGAAGCGTACCT 817
Db 421 ttttattaccgtatgccaacatttgccttcacatcatgaacttcagagagacctagct 480
Qy 818 ACAGACTATCTTCAGCTGATGCTGTATGCTTTAAACACGAGCATCAAAATCCCAAGTTCT 877
Db 481 acagatattcttcaactaatggtgtaagtcactaaaaccagcatcaaaatcccaagtct 540
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CC activity, and screening for receptors to OBM which mediate its function.
CC These substances can then be used in the treatment of disorders of bone
CC function and calcium metabolism. The antibodies can be used for assay
CC of the protein, for investigative and diagnostic purposes, and as
CC components of drugs.
XX
XX

SQ Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;

Query Match 43.4%; Score 951; DB 19; Length 951;
Best Local Similarity 100.0%; Pred. No. 6e-214;
Matches 951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 ATGCCCGCGGCGGAGAGACTACGGGAAATACCTGCGGAGTTCGGAGAGATGGGCGAGC 184
Db 1 atgcgcggcgccagccgagactacggcaat; tacctgcgcagctcgaggagatggcgagc 60
Qy 185 GCGCCCGCGCTCCACACAGAGGTCGCGTACACCCGCGCTTCCTGACCGGCTCCGCGG 244
Db 61 ggcgcggcgctccacacaggggtccgct; jcaccgcgcgcctctgcaccggcgtccgcg 120
Qy 245 CCGCACCGCGCGCTCCGCTCCATGTTCTGCGCCCTCCTGGGCTGGGAGTGGCCGAG 304
Db 121 cgcacaccgcgcctccgctccatgttctgcgcctctgggctgggactgggcccag 180
Qy 305 GTGGTCTCAGATCGCTCTGTTCCTGTAATTTAGATCTTCAGACTCCATCAAAACGCGTTTG 364
Db 181 gtggtctcagcatcgtctgtctctgtacttctgagcgcagatggtatcctaacaagaata 240
Qy 365 TCAGAAGACAGACTCAGCTCTTTTATAGATCTTCAGACTCCATCAAAACGCGTTTG 424
Db 241 tcagaagacagactcaactgttttatagatctctgagactccatgaaacagaggttg 300
Qy 425 CAGACTCGACTCTGGAGAGTGAACACACTACCTGACTCTCTGCGCCACAGCGCTTCTCA 484
Db 301 caggactcgaactctggagagtgaagacacactacactgactctcgcaggaggtgaacaa 360
Qy 485 GCCTTTCAGGGGCGCGTGCAGAGGAAGTCAACACATTTGGGCGCCACAGCGCTTCTCA 544
Db 361 gcccttcaggggcgctgcagaggaactgcaacacattgtgggcccacagcgtcttca 420
Qy 545 GGAGTCCAGCTATGATCGAAGGCTCATGTTGGATGTGGCCCGCCAGCGGCAAGCCTGAG 604
Db 421 ggagctcagctatgatggaaggctcatggttgatgtggccacgagggcaagcctgag 480
Qy 605 GCCAGCCATTTGCACACTCAGCATCAATGCTGCGCAGCATCCCATCGGTTCCCATAAA 664
Db 481 gccagccatttgcacactcaccatcaatgctgcagcatcccatcggttcccataaa 540
Qy 665 GTCACTCTGCTCTTGTGATCAGCATCGAGGCTGGGCGCAAGATCTTAACATGACGTTA 724
Db 541 gtaactctgtcctctgtgtaccagatcagagctgggcccagatctcaacatgacgtta 600
Qy 725 AGCAACGAAAGAACTAAGGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCCAACATTTGC 784
Db 601 agcaacgaaactaaaggttlaaccaagatggcttctattaccctgtacgccaaacttgc 660
Qy 785 TTTGGCATATGAACATCGGAGGCTACCTAGACACTATCTCAGCTGATGTGTAT 844
Db 661 ttctggcaatcagaaactcgggaagcgtacctacagactatcttcagctgagtgtat 720
Qy 845 GTCGTTAAACAGCATCAAAATCCCAAGTTCTCATACCTGATGAAAGGAGGAGGACAG 904
Db 721 gctgtaaacacagcatcaaaatcccaagttctcataacctgaagaaaggaggagcag 780
Qy 905 AAAAAGTGGTGGGCAATTCGAATTCCTTTTATTCCTCAATATGTTGGGGATTTTTC 964
Db 781 aaaaactggtcggaattctgaattccacttttattccataaaatgttggggatttttc 840
Qy 965 AAGTCCGAGCTGTGAGAAATATAGCATCAGGTGTCCACCCCTTCCTGCTGTGATCCG 1024
Db 841 aagctccgagctgttgaagaataatagcat; tcaggtgttccaaaccttccctgctgagctcg 900

Qy 1025 GATCAAGATCGGACGACTACTTTGGGCTTTCAAAGTTTCAGGACATAGACTGA 1075
Db 901 gatcaagatcgacagctactttggggttttcaaagtttcaggacatagactga 951

RESULT 12

ID Z99965 standard; DNA; 951 BP.

XX Z99965;

DT 25-JUL-2000 (first entry)

XX DNA encoding a murine osteoprotegerin ligand (OPGL).

XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.

OS Mus musculus.

XX Key Location/Qualifiers
FH CDS 1..951

FT /*tag= a
/product= "osteoprotegerin ligand"

XX WO200015807-A1.

XX PD 23-MAR-2000.

XX PF 13-SEP-1999; 99WO-DK00481.

XX PR 15-SEP-1998; 98DK-0001164.

XX PR 02-OCT-1998; 98US-0102896.

XX (MEBI-) M & E BIOTECH AS.

XX Halkier T, Heaning J;

XX WPI: 2000-271444/23.

XX P-PSDB; Y84418.

XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used

XX to treat, prevent and ameliorate osteoporosis -

XX Disclosure: Page 79-81; 110pp; English.

XX The present sequence encodes a murine osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.

XX Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;

Query Match 43.4%; Score 951; DB 21; Length 951;
Best Local Similarity 100.0%; Pred. No. 6e-214;
Matches 951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 ATGCCCGCGGCGGAGAGACTACGGGAAATACCTGCGGAGTTCGGAGAGATGGGCGAGC 184
Db 1 atgcgcggcgccagccgagactacggcaat; tacctgcgcagctcgaggagatggcgagc 60

QY 185 GGCCCGGGCTCCACACAGAGGGTCCGCTGCACCCGCGCTTCTGCACCGGCTCCGCGC 244
DB 61 gggcccgggctccacacagggctccgctgcaccccgcgctctctgaccggtcccgcg 120
QY 245 CGCCACCGCGCCCTCCCGCTCCATGTTCTCTGCGCCCTCTGGGGCTGGGACTGGGCGAG 304
DB 121 cggccacggcgccctcccgctccatgttctggtgcccctctgggctgggactgggcccag 180
QY 305 GTGGTCTGCAGCATCGCTCTGTGTTCTGTACTTTCGAGCGCAGATGATCTTAACAGAAATA 364
DB 181 gtggtctgcagcatcgctctgttctgtacttttcgagcgcagatggatctctaacaagaata 240
QY 365 TCAGAGACAGCACTCAGCTCTTTTATAGAAATCCTGAGACTCCATGAAAGCGCAGGTTTG 424
DB 241 tcagaagacagcactcagctgttttatagaatcctgagactccatgaaaacgcagggttg 300
QY 425 CAGGACTCGACTCTGGAGAGTGAAGACACACTACTGACTTCCTGCAGGAGGATGAACAAA 484
DB 301 caggactcgacttgagagtgaagacacactacctgactctcgaggaagatgaaacaa 360
QY 485 GCCTTTACGGGGCCGTGCGAGAGAACTGCAACACATTTGTGGGGCCACAGCGCTTCTCA 544
DB 361 gcccttcagggggcccgtgcagaagaaactgcaacacattgtggggccacagcgcttctca 420
QY 545 GGAGCTCCAGCTATGATGGAGAGCTCATGGTTGGATGTGGCCCGCAGCGCAGCAAGCCTGAG 604
DB 421 ggaagctccagctatgatggaagctcatggttgatgtggcccgagggcaagcctgag 480
QY 605 GCCAGCCATTTGCACACCTTCACCATCAATGCTGCCAGCATCCATCGGGTCCCATATAA 664
DB 481 gccagccatttgcacaccltccactcaatcaatgctgcagcatccatcggtttcccataa 540
QY 665 GTCACTCTGTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAATCATGACCTTA 724
DB 541 gtcaactctgtctcttggtaccacgatcgagctgggccaagatctcttaacatgacgtta 600
QY 725 AGCAACGGAAACTAGGGTTACCAAGATGGCTTCTATTACCTGTACGCCACACATTTGC 784
DB 601 agcaacggaaaactaagggttaccacgaagtggcttctattacactgtacgcacacatttgc 660
QY 785 TTTTCGGCATCATCAACATCGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT 844
DB 661 ttctcgcaatcatgaacacatcggaagcgtacctcacagactatcttcagctga1ggtgat 720
QY 845 GTCGTTAAACACAGCATCAAAATCCCAAGTTCTCATAACTGATGAAAGGAGGAGCAGC 904
DB 721 gtcgttaaaacacagatcaaaatcccgaagttctcataaacctgatgaaaggaggagcaag 780
QY 905 AAAAATGGTCGGGCAATTCTGAAATCCCACTTTTATTCATAAATGTTGGGGATTTTTC 964
DB 781 aaaaactggtcggggcaattctgaattccacttttattccataaatgttg9gggatttttc 840
QY 965 AAGCTCCGAGCTGGTGAGAAATAGCATTCAGGTGTCGAACCTTCCCTGCTGGATCCG 1024
DB 841 aagctccgagctggtgaagaaattagcattcagggtgtccaaccttccctgctggatccg 900
QY 1025 GATCAAGATCGCAGCTACTTTTGGGGCTTTTCAAAGTTTCAGGACATAGACTGA 1075
DB 901 galcaagatgcagcgtactttg9gggttttccaaagtttcaggacatagactga 951

RESULT 13
ID 249024
XX 249024 standard; DNA; 951 BP.
AC 249024;
XX
DT 31-MAR-2000 (first entry)
XX
DE Osteoclast formation promoting factor coding sequence.
XX
KW OBM-BP; OBM binding protein; osteoclast formation promoting factor;

bone metabolic disease; osteoporosis; therapy; ss.
Mus sp.
JPL132581-A.
07-DEC-1999.
20-OCT-1998; 98JP-0316973.
24-MAR-1998; 98JP-0076232.
(SNOW) SNOW BRAND MILK PROD CO LTD.
(SANY) SANKYO CO LTD.
WPI; 2000-091362/08.
A new protein, a DNA and its application -
Example 1; Page 13; 18pp; Japanese.
XX
CC This sequence encodes the osteoclast formation promoting factor (OBM).
CC The invention relates to an OBM binding protein (OBM-BP). The protein is
CC useful as a preventive and/or treating agent for bone metabolic diseases
CC such as osteoporosis. Substances which inhibit the binding of OBM to
CC OBM-BP can be used as biochemical reagents.
XX
SQ Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;

Query Match 43.4%; Score 951; DB 21; Length 951;
Best Local Similarity 100.0%; Pred. No. 6e-214;
Matches 951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 ATGCGCGGGCCAGCGGAGCTACGGCAAGTACCTGCGCAGCTCGAGGAGATGGGCAGC 184
DB 1 atgcgcggggccagcgagactacgcgcaagtaccttcgcagctcgagagatgggcagc 60
QY 185 GGCCCGCGCTCCACACAGAGGTCGCTGCACCCGCGGCTTCTGCACCGGCTCCGGCG 244
DB 61 ggccccggcgtccacacagagggtccgctgcaccccgcgcttctgcacggctccggcg 120
QY 245 CGCGACCGCGCGCTCCCGCTCCATGTTCTGTGGCCCTTCCTGGGGCTGGGACTGGGCCAG 304
DB 121 ccgcacacgcgcctcccgctccatgttctgacctctggtggtggtggtggtggtggtg 180
QY 305 GTGCTCTGCAGCATCGCTCTGTCTCTGTACTTTCGAGCGCAGATGATCTTAACAGAAATA 364
DB 181 gtgctctgcagcatcgctctgttctctgtactttcagcgcagatggatcttaacagaata 240
QY 365 TCAGAAGACAGCACTCACTGCTTTTATAGAAATCCTTCAGACTCCATGAAACGACAGTTTG 424
DB 241 tcagaagacagcactcactgcttttatagaatcctgagactccatgaaaacgcagggttg 300
QY 425 CAGGACTCGACTCTGGAGAGTGAAGACACACTACTGACTCTCTGCAGGAGGATGAACAAA 484
DB 301 caggactcgactctggagagtgaagacacactacactgactctgagggagatgaaacaa 360
QY 485 GCCTTTACGGGGCGCTGCAGAGAACTGCAACACATTTGTGGGCCACAGCGCTTCTCA 544
DB 361 gcccttcagggggcccgtgcagaagaaactgcaacacattgtg9ggccacagcgttctca 420
QY 545 GGAGCTCCAGCTTATGATGGAAGGCTCATGTTGGATGTGGCCCGCAGCGAGGCTGAG 604
DB 421 ggaagctccagctatgatggaagctcatggttgatgtggcccgagggcaagcctgag 480
QY 605 GCCAGCCATTTGCACACCTTCACCATCAATGCTGCCAGCATCCATCGGGTCCCATATAA 664
DB 481 gccagccatttgcacaccltccactcaatcaatgctgcagcatccatcggtttcccataa 540
QY 665 GTCACTCTGTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAATCATGACCTTA 724
DB 541 gtcaactctgtctcttggtaccacgatcgagctgggccaagatctcttaacatgacgtta 600

QY 725 AGCAACGGAAACTAAGGGTTAACCAAGTGGCTTCTATTACCTGTACGCCAACATTTCG 784
 Db 601 agcaacggaactaagggttaaccaagctggcttctattactgtacgccaacatttgc 660
 QY 785 TTTTCGGCATCATGAACATPCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGAT 844
 Db 661 ttctggcatcatgaacaacggaagcgtacctacagactatcttcagctgagtgat 720
 QY 845 GTCTGTTAAACACGATCAAAATCCCAKTTCTCTAATACCTGATGAAGGAGGAGCACG 904
 Db 721 gtcgttaaaccagatcaaaatcccaatctctataacctgatgaagagagggagcacg 780
 QY 905 AAAAATGCTCGGGCAATTCGAATTCCTCTTTTATTCATATAATGTTGGGGGATTTTC 964
 Db 781 aaaaactgctcgggcaattctgaattccrctttattccataaatgttggggatttttc 840
 QY 965 AAGCTCCGAGCTGGTGAAGAAATTAGCACTCAGGTGTCTCAACCTTCCCTGCTGGATCCG 1024
 Db 841 aagctccgagctggtagaagaattagcatcagggtgccaaaccttccctgctggatccg 900
 QY 1025 GATCAAGATGCCACGTACTTTGGGGCTTCAAAGTTTCAGGACATAGACTGA 1075
 Db 901 gatcaagatgcgactactcttggggcttcaaaagttcaggacatagactga 951

RESULT 14
 V69898
 ID V69898 standard; CDNA to mRNA; 731 BP.
 XX V69898;
 AC
 CC
 DT 10-FEB-1999 (first entry)
 XX
 DE Nucleic acid encoding a murine OCIF-binding molecule (OBM).
 XX
 KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption facto.; bone disorder; calcium metabolism;
 KW mouse; ss.
 OS
 XX Mus sp.
 XX
 FH Key
 FT CDS
 FT 1..735
 FT /*tag= a
 XX
 PN W09846644-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-JP01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO L'ID.
 XX
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shimada N, Takahashi T, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 XX
 DR WPI: 1998-594563/50.
 DR P-PSDB: W83019.
 XX
 XX Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 XX
 PS Example 28; Page 121; 151pp; Japanese.
 XX

CC The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 XX
 SQ Sequence 735 BP; 205 A; 182 C; 179 G; 169 T; 0 other;

Query Match 33.5%; Score 735; DB 19; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.7e-163;
 Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 GCCCAGATGCCTTACAGATATCAGAAAGACGACTCCTGCTTTTATAGAACTCCTG 400
 Db 1 gcccagatggtcttaacagaaatcagaagacgactcactgcttttatagaatcctg 60

QY 401 AGACTCCATGAAACGCAGGTTTGCAGGACTCGACTCTGGAGAGTGAAGACACACTACT 460
 Db 61 agactccatgaaacgcagggttgcaggactcgtgagagtgagagtcactacactacct 120

QY 461 GACTCTCGAGGAGATGAACAAAGCCTTTTCAGGGGCCCTGCAGAAAGAACTGCAACAC 520
 Db 121 gactcctcgaggagatgaacaagcctttcaggggccgtcgagaaggaactgcaaacac 180

QY 521 ATTGTGGGCCACAGCGCTTCTCAGGAGCTCCAGCTATGATGAAGGCTCATGTTGGAT 580
 Db 181 attgtgggccaagcgctcttcaggagctccagctatgatgaaaggctcagtggtgat 240

QY 581 GTGGCCCGGAGGCAAGCCTGAGGCCAGCCATTTGCACACCTCACCATCAATGCTGCC 640
 Db 241 gtggcccgagggcaagcctgagggccagccatttgcacacccactcaaatgctgcc 300

QY 641 AGCATCCCATCGGGTCCCATATAAGTCACTCTGTCTCTTGGTACCACGATCGAGGCTGG 700
 Db 301 agcatcccatcggggtcccatataagtcactctgtcctcttgggtaccacgactcgaggctgg 360

QY 701 GCCAAGATCTTAACATGAGCTTTAAGCAACGAAACTTAAGGGTTAACCAAGATGGCTTC 760
 Db 361 gccaaagtcttaacatgacgtttaagcaacggaaaactaagggttaaccaagatggcttc 420

QY 761 TATTACCTGTACGCCAACATTTGCTTTTCGGCATCATGAACATCGGGAGCGTACCTTACA 820
 Db 421 tattacctgtacgccaacatttcttcggcatcatgaacaatcggaagcgtacactaca 480

QY 821 GACTATCTTCAGCTGATGGTGATGCTGTTAAACACGAGCATCAAAATCCCAAGTTCAT 880
 Db 481 gactatcttcagctgattggtgtgtgtcggttaaacacacgacatcaaaatcccaagcttccat 540

QY 881 AACCTGATGAAGGAGGAGGACGACGAAAACTGGTTCGGGGCAATTTCTGTAATTCACCTTTAT 940
 Db 541 aacctgatgaagagggagcagcaaaaaactggtcgggcaattctgaattccacttttat 600

QY 941 TCCATAAATGTTGGGGGATTTTCAAGCTCCGAGCTGGTGAAGAAATATGACATTTCAGGTG 1000
 Db 601 tccataaatgttgggggatttttcaagctccgagctggtgaagaaaattagcatttcaggtg 660

QY 1001 TCCAACCTTCCCTGCTGGATCCGATCAAGATGCCAGCTACTTTGGGGCTTCAAAAGTT 1060
 Db 661 tccaaaccttccctgctggatccggtatcaagatgcgacttcttggggcttccaaagtt 720

QY 1061 CAGGACATAGACTGA 1075
 Db 721 caggacatagactga 735

RESULT 15
V41378
ID V41378 standard; cDNA; 954 BP.
XX
AC V41378;
XX
DT 08-OCT-1998 (first entry)
XX
XX NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
DE
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..954
FT
FT /*tag= a
FT /product= "human RANKL (ligand for RANK)"
XX
XX W09828426-A2.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-US23775.
XX
PR 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
XX (IMNV) IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
PI
DR WPI: 1998-377657/32.
DR P-PSDB; W69957.
XX
XX New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells
XX
XX Claim 25; Pages 59-60; 80pp; English.
XX
XX This cDNA encodes a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening.
XX
SQ Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

Query Match 30.4%; Score 666.2; DB 19; Length 954;
Best Local Similarity 82.5%; Pred No. 4.2e-147;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

QY 125 ATGGCCGGCCGACGCGAGAGTACGGCAAGTACCTGCCAGCTCGGAGGAGATGGGCGAC 184
D 1 atgcccgcgcagcagagactacaccaagtacctggtgctcgaggagatggcgccg 60
QY 185 GGGCCCGCGCTCCACACAGAGGTCGCTGCACCCCGCGCTTCTGCACCCGCTCCGGCG 244
D 61 gcccgc 117
QY 245 CCGCCACCCCGCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCT 304
D 118 cagcccccgc 177
QY 305 GTGGTCTGCAGCATCGCTCTGTTCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 364
D 178 gttgtctgcagcgtcgccctgttcttcttcttcttcttcttcttcttcttcttcttctt 237
QY 365 TCAGAGACAGCAGCTACT 424
D 238 tcagaagatggcactcactcactcactcactcactcactcactcactcactcactcactcact 297
QY 425 CAGGACTCGACTCTGGAGAGTGAACACACACACACACACACACACACACACACACACAC 478
D 298 caagacacactctggagagtgcaagatacaaaaattacattacattacattacattacattac 357
QY 479 AACCAAGCCTTTTCAGGGGGCGGTGCAGAGAACTGCACACATTTGTTGGGCCAGGCGC 538
D 358 aacagggccttcaaggagctgtgcaaaaggaattacaacatatctgttggatccacagcac 417
QY 539 TTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGGTTGGTTGGTTGGTTGGTTGGTTGG 598
D 418 atcagagcagagaaacgagtggtggtggtggtggtggtggtggtggtggtggtggtggtg 477
QY 599 CCTGAGGCCGACCTTTCACACCTCACCATCAATGTCGTCGTCGTCGTCGTCGTCGTCGTC 658
D 478 ctggaagctcagcccttctgctcactcactcactcactcactcactcactcactcactcact 537
QY 659 CATAAAGTCACTCTGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 718
D 538 cataaagtgcgtct 597
QY 719 ACGTTAGCAGCAGCAAACTAAGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCAC 778
D 598 acttttagcaatggaaaactaatagtaatacagagtggttcttattacctgtatgccaac 657
QY 779 ATTTGCTTTCGGCATCATGAACATCGGCAAGCTACAGACTATCTTCAGCTGATG 838
D 658 attgcttctcagacatcatgaaacttcaggagacctagctacagagatatcttcaactaag 717
QY 839 GTGTATGTCGTTAAACACAGCATCAAAATCCCAAGTCTCTCAATACCTGATGAAGAGGG 898
D 718 gtgtactcactaaaaccagcatcaaaatcccaagttctcactcactcactcactcactcactc 777
QY 899 AGCAGCAAAACTGGTCGGGCAATCTGAAATCCACTTTTATTCATTAATGTTGGGGA 958
D 778 agcaccagtatggctcaggggaattctgaattctcatttttttttttttttttttttttttt 837
QY 959 TTTTTCAGCTCCAGCTGGTGACAAATAGCATTCAGGTGTCACACCTTCCTTCCTTCCTG 1018
D 838 ttttttaagtctacggtctggagaggaatcctgaattctcatttttttttttttttttttttt 897
QY 1019 GATCCGATCAAGATCGGACCTACTTTTGGGCTTTTCAAGTTCAGGACATAGACTGA 1075
D 898 gatccgagcaggtgcaacatacttttgggctttttaaagttcgagatatagattga 954

Search completed: December 28, 2000, 19:38:01
Job time: 6736 sec

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OM nucleic - nucleic search, using sw model

Run on: December 28, 2000, 17:40:57 ; Search time 147.31 Seconds
(without alignments)
2249.467 Million cell updates/sec

Title: US-08-989-362-1
Perfect score: 2191
Sequence: 1 GCCAGGACCTCTGTGAACG.....TTTGGTACTTAAATGCG 2191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/5C.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/5D.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/6.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq: *
7: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2144.8	97.9	2295	3	US-08-842-842-6
2	1615.8	73.7	1630	5	US-08-996-139-10
3	666.2	30.4	954	5	US-08-996-139-12
4	58.4	2.7	1042	5	US-08-584-031-2
5	58.4	2.7	1042	5	US-08-780-496-2
6	58.4	2.7	1521	2	US-08-670-354-3
7	58.4	2.7	1521	6	PCT-US96-10895-3
8	58.4	2.7	1751	2	US-08-670-354-1
9	58.4	2.7	1751	6	PCT-US96-10895-1
10	54	2.5	1366	6	PCT-US96-10895-5
11	54	2.5	1366	6	PCT-US96-10895-5
12	51.4	2.3	8220	4	US-08-568-459A-11
13	51.4	2.3	8220	4	US-08-487-826B-11
14	51.4	2.3	19124	4	US-08-487-826B-13
15	45.8	2.1	19124	4	US-08-487-826B-13
16	44.4	2.0	4257	3	US-08-690-473-1
17	44.4	2.0	12001	2	US-08-458-568A-11
18	43.4	2.0	4616	2	US-08-340-203A-1
19	43.4	2.0	4616	3	US-08-452-567-1
20	43.4	2.0	4616	4	US-08-452-427-1
21	43.4	2.0	4616	5	US-09-085-407-1
22	43.4	2.0	6243	4	US-09-056-075-1
23	42.4	1.9	2960	5	US-08-913-842-3
24	42.4	1.9	8920	3	US-08-446-855A-1
25	42	1.9	5117	5	US-08-854-585-1
26	42	1.9	5117	6	PCT-US95-05512-1

C 27	41.4	1.9	6768	2	US-08-107-755A-1	Sequence 1, Appli
C 28	41.4	1.9	8457	1	US-07-991-867B-1	Sequence 1, Appli
C 29	41.4	1.9	8457	4	US-08-544-332-1	Sequence 1, Appli
30	41	1.9	991	5	US-08-924-747-25	Sequence 25, Appli
31	40.8	1.9	2015	5	US-08-633-993A-30	Sequence 30, Appli
32	40.6	1.9	1120	5	US-09-030-613-1	Sequence 1, Appli
C 33	40.4	1.8	1422	2	US-08-319-704-5	Sequence 5, Appli
C 34	40.4	1.8	3095	7	5231168-1	Patent No. 5231168
C 35	40.2	1.8	2621	4	US-08-553-619B-8	Sequence 8, Appli
C 36	40.2	1.8	2897	4	US-08-927-394-1	Sequence 1, Appli
C 37	40.2	1.8	5852	1	US-07-867-106-2	Sequence 2, Appli
38	40.2	1.8	246240	3	US-08-724-394A-20	Sequence 20, Appli
39	40.2	1.8	246240	3	US-08-724-394A-21	Sequence 21, Appli
40	40.2	1.8	246240	3	US-08-724-394A-22	Sequence 22, Appli
C 41	40	1.8	2070	2	US-08-486-342-1	Sequence 1, Appli
C 42	40	1.8	2070	2	US-08-473-092-1	Sequence 1, Appli
C 43	40	1.8	2070	2	US-08-614-801A-1	Sequence 1, Appli
C 44	40	1.8	2076	2	US-08-066-371-1	Sequence 1, Appli
C 45	40	1.8	2076	6	PCT-US94-05666-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-842-842-6
; Sequence 6, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: OSTEOCALCIN BINDING PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91230-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,842
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2295 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 158...1105
US-08-842-842-6

Query Match	97.9%	Score 2144.8	DB 3	Length 2295
Best Local Similarity	99.4%	Pred. No. 0		
Matches 2174	Conservative 0	Mismatches 12	Indels 2	Gaps 2
Qy 1	GCAGGACCTCTGTGAACCGTGGGGGGCGCGCTGGCGGGGACTCTGCTCGCGG	60		
Db 34	GCAGGACCTCTGTGAACCGTGGGGGGCGCGCTGGCGGGGACTCTGCTCGCGG	93		
Qy 61	TGGGTGGCGGAGGAGGAGAGAACGATCGGGAGCGGCGCCGGAATCCCGGCGCG	120		

[illegible]

RESULT 2
US-08-996-139-10

25

Sequence 10, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY:
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
US-08-996-139-10

Query Match 73.7%; Score 1615.8; DB 5; Length 1630;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 189 CCGGCGTCCACACGAGGGTCCGCTGACCCCGCGGCTTCTGCACCGGCTCCGGGGCGGC 248
Db 1 CCGGCGTCCACACGAGGGTCCGCTGACCCCGCGGCTTCTGCACCGGCTCCGGGGCGGC 60
QY 249 CACCGCGCGGCTCCCGCTCCATGTTCTGCGCCCTCCCTGGGCTGGGACTGGGCGAGGTGG 308
Db 61 CACCGCGCGGCTCCCGCTCCATGTTCTGCGCCCTCCCTGGGCTGGGACTGGGCGAGGTGG 120
QY 309 TCTGCAGCATCGTCTGTCTCTGTACTTTCGAGCGCAGATGGATCCTTAACAGAAATATCAG 368

Db 121 TCTGCAGCATCGTCTGTCTCTGTACTTTCGAGCGCAGATGGATCCTTAACAGAAATATCAG 180
QY 369 AAGACAGCACTCACTGCTTTTATAGAATCTTGAGACTCCATGAAACACGAGTTTGCAGG 428
Db 181 AAGACAGCACTCACTGCTTTTATAGAATCTTGAGACTCCATGAAACACGAGTTTGCAGG 240
QY 429 ACTCGACTCTGGAGAGTGAAGACACACTACTGACTCTCTGAGGAGGATGAACAGGCT 488
Db 241 ACTCGACTCTGGAGAGTGAAGACACACTACTGACTCTCTGAGGAGGATGAACAGGCT 300
QY 489 TTCAGGGGGCGGTGCAAGAAGAACTGCAACACATTGTGGGCCACAGCGCTTCTCAGAG 548
Db 301 TTCAGGGGGCGGTGCAAGAAGAACTGCAACACATTGTGGGCCACAGCGCTTCTCAGAG 360
QY 549 CTCAGCATATGATGGAGGCTCATGTTGGATGTGGCCACGAGGCAAGCTGAGGCC 608
Db 361 CTCAGCATATGATGGAGGCTCATGTTGGATGTGGCCACGAGGCAAGCTGAGGCC 420
QY 609 AGCCATTTCACACCTCACCATCAATGCTGCCAGCATCCCATGGGTTCCCATAAAGTCA 668
Db 421 AGCCATTTCACACCTCACCATCAATGCTGCCAGCATCCCATGGGTTCCCATAAAGTCA 480
QY 669 CTCTGCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAAACATGACGTTAAGCA 728
Db 481 CTCTGCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAAACATGACGTTAAGCA 540
QY 729 ACGGAAACCTAAGGTTTAAACAAGATGGCTTCTATTACCTGTCACGCAACATTTGCTTTC 788
Db 541 ACGGAAACCTAAGGTTTAAACAAGATGGCTTCTATTACCTGTCACGCAACATTTGCTTTC 600
QY 789 GGCATCATGAACATCGGGAAGGCTACTACAGACTATCTTTCAGCTGATGGTGTATGTCG 848
Db 601 GGCATCATGAACATCGGGAAGGCTACTACAGACTATCTTTCAGCTGATGGTGTATGTCG 660
QY 849 TTAACACACGATCAAAATCCCAAGTTCTCATACCTGTGAAGAGGAGGACGAGGAAA 908
Db 661 TTAACACACGATCAAAATCCCAAGTTCTCATACCTGTGAAGAGGAGGACGAGGAAA 720
QY 909 ACTGGTCGGGCAATCTGAAATTCACATTTTATTCCATAAATGTTGGGGATTTTTCAGG 968
Db 721 ACTGGTCGGGCAATCTGAAATTCACATTTTATTCCATAAATGTTGGGGATTTTTCAGG 780
QY 969 TCGAGCTGGTGAAGAAATTAGCATTACAGGTGTCAACACCTTCCCTGCTGGATCCGGATC 1028
Db 781 TCGAGCTGGTGAAGAAATTAGCATTACAGGTGTCAACACCTTCCCTGCTGGATCCGGATC 840
QY 1029 AGATCGGAGGTACTTTGGGGCTTTCAAAGTTTCAGGACATAGACTGAGACTCATTTCGTG 1088
Db 841 AAGATCGGAGGTACTTTGGGGCTTTCAAAGTTTCAGGACATAGACTGAGACTCATTTCGTG 900
QY 1089 GAACATTAGCATGGATGCTCTAGATGTTTGGAAACTTCTTAAAAAATGGATGATCTAT 1148
Db 901 GAACATTAGCATGGATGCTCTAGATGTTTGGAAACTTCTTAAAAAATGGATGATCTAT 960
QY 1149 ACATGTGAAGACTACTAAGAGACATGGGCCACCGGTATGAAACTCACAGCCCTCTCTC 1208
Db 961 ACATGTGAAGACTACTAAGAGACATGGGCCACCGGTATGAAACTCACAGCCCTCTCTC 1020
QY 1209 TTGAGCCTTACAGGTTGTATATATGTAAGTCCATAGGTGATGTTAGATTCATGGTAT 1268
Db 1021 TTGAGCCTTACAGGTTGTATATATGTAAGTCCATAGGTGATGTTAGATTCATGGTAT 1080
QY 1269 TACACAAACGGTTTACAAATTTTCTAATGATTTCTTAAGAAATGAACAGATTTGGGAGG 1328
Db 1081 TACACAAACGGTTTACAAATTTTCTAATGATTTCT - AGAATTGAACAGATTTGGGAGG 1139
QY 1329 TATTCGAGTCTTATGAAAAAATTCACAGGTGAGCTATGGAAGGGGTTCACAGTCTCTGGG 1388
Db 1140 TATTCGAGTCTTATGAAAAAATTCACAGGTGAGCTATGGAAGGGGTTCACAGTCTCTGGG 1199
QY 1389 TCTAACCCCTGGACATGTGCCACTGAGAACCTTGAATTAAGAAAGATGCCATGTCATTGC 1448

Db 1200 TCTAACCCCTGGACATGTGCCACTGAGACCTTGAANAATAAGAGATGCCATGTCTATGC 1259
QY 1449 AAAGAAATGATAGTGTGAAGGGTTAACT'CTTTTGAATTGTTACATTCGCGCTGGACCTG 1508
Db 1260 AAAGAAATGATAGTGTGAAGGGTTAACT'CTTTTGAATTGTTACATTCGCGCTGGACCTG 1319
QY 1509 CAATAGATCTTTTCTCTTAAGTGAAGAAGAGAAATATATGATATTTTATATATGTCT 1568
Db 1320 CAATAGATCTTTTCTCTTAAGTGAAGAAGAGAAATATATGATATTTTATATATGTCT 1379
QY 1569 AAAGTATATTTTCAGSGTGAATGTTTC'GTGCAAAAGTTTGTAAATATATATTTGTGCTA 1628
Db 1380 AAAGTATATTTTCAGSGTGAATGTTTC'GTGCAAAAGTTTGTAAATATATATTTGTGCTA 1439
QY 1629 TAGTATTTGATTCAAAATATTTTAAATAT'CTCTCACTCTTGACATATTAATGTTTTTAAAT 1688
Db 1440 TAGTATTTGATTCAAAATATTTTAAATAT'CTCTCACTCTTGACATATTAATGTTTTTAAAT 1499
QY 1689 GTACAGATGATTTTAACTGTGTGACACTTT'TAATTCCTCTGAAGGTACTCGTAGCTAAAGG 1748
Db 1500 GTACAGATGATTTTAACTGTGTGACACTTT'TAATTCCTCTGAAGGTACTCGTAGCTAAAGG 1559
QY 1749 GGCAGAAATAGTCTTCTGTTGAGCACATAT'TAGTTTATTTCTTTTATTTCTTTTAACTTAAT 1808
Db 1560 GGCAGAAATAGTCTTCTGTTGAGCACATAT'TAGTTTATTTCTTTTATTTCTTTTAACTTAAT 1619
QY 1809 AGACTCTTTCAG 1819
Db 1620 AGACTCTTTCAG 1630

RESULT 3

US-08-996-139-12
; Sequence 12, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/061,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/811,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 954'base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: huRANKL (full length)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; US-08-996-139-12

Query Match 30.4%; Score 666.2; DB 5; Length 954;
Best Local Similarity 82.5%; Pred. No. 2e-153;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

QY 125 ATGCGCGCGGCGCAGCCGAGACTACGGCAAGTACCTGCGCAGCTCGGAGGAGATGGGCAGC 184
Db 1 ATGCGCGCGGCGCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGCGGC 60
QY 185 GGCCCGCGGCTCCACACGAGGCTCGCTGCACCCCGCGCTTCGCACCGGCTCCGGCG 244
Db 61 GGCCCGGAGCCCGCAGGCGCCCTGCACGCCCGCGC---CGCGCGCTCGCGCGCAC 117
QY 245 CGCGCACCGCGCGCTCCCGCTCCCATGTTCTTGGCCCTCTCGGGCTGGGACTGGGCCAC 304
Db 118 CAGCCCGCGCGCTCCCGCTCCCATGTTCTGTTGGCGCTCTCGGGCTGGGCCAG 177
QY 305 GTGCTCTGCAGCATCGCTCTGTTCTGTTCTTCCAGCGCAGATGATGATTAACAGATA 364
Db 178 GTTGTCTGCAGCGTCCCGCTCTGTTCTTCTTTCAGAGCGCAGATGATGATTAAGAATA 237
QY 365 TCAGAAAGACAGCATCTACTGCTTTTATAGAATCTCTGAGACTCCATGAAACCGAGTTTG 424
Db 238 TCAGAAAGATGGCATCTACTGCTTTTATAGAATTTTGGAGACTCCATGAAATCGAGATT 297
QY 425 CAGGACTCGACTCTGGAGAGTGAAGACAC-----ACTACCTGACTCTCTGCAGGAGGATG 478
Db 298 CAAGACACACTCTGGAGAGTCAAGATACAAAAATTAATACCTGATTCATGTAGGAGAAAT 357
QY 479 AAACAAGCCTTTTCAGGGGCGGTGCGAAGAACTGCAACACATTTGTGGGGCCACAGCGC 538
Db 358 AAACAGCGCTTTTCAGGAGCTGTGCAAAAGGAATTTACAACATATCTGTTGGATCACAGCAC 417
QY 539 TTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCCAGGAGGCAAG 598
Db 418 ATCAGAGCAGAGAAAGCGATGTTGGATGCTCATGTTAGATCTGCCCAAGAGGAGCAAG 477
QY 599 CCTGAGGCGCCAGCATTTTGCACACTCCACATCAATGTCTGCCAGCATCCCATCGGTTTCC 658
Db 478 CTTGAAGCTCAGCGCTTTTGTCTCATCTCATATAATATGTCACCGACATCCCATCTGGTTCC 537
QY 659 CATAAAGTCACTCTGCTCTTGTGTACACGATCCAGGCTGGGCCAAGATCTCTTACATG 718
Db 538 CATAAAGTGAAGTCTGCTCTTGTGTACCATGATCGGGTGTGGGCCAAGATCTTCCAACTG 597
QY 719 ACCTTAAACAACGGAATAAGGTTTAAACCAAGATGGCTTCTATTTACTGTACGCCAAC 778
Db 598 ACTTTTAGCAATGGAATAACTAATAGTTAATCAGGATGGCTTTTATAGCTGTATGCCAAC 657
QY 779 ATTTGCTTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCACTGATG 838
Db 658 ATTTGCTTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGACTATCTTCAACTAATG 717
QY 839 GTGTATGTCTGTAAACACGATCAAAATCCCAAGTTCTCATACCTGATGAAGAGGG 898

Db	718 GTGTGCTCACTAAACAGCATCAAAATCCCAAGTTCTCATACCCTGAAGAAGGAGGA	777
QY	899 AGCACAAAACACTGGTCGGCCAATTCTCAATTCACATTTTTATTTCCATAAATGTTGGGGGA	958
Db	778 AGCACAAGTATTGGTCAGGGAATTTCTGAATTCATTTTTATTTCATAAACGTTGGTGGA	837
QY	959 TTTTTCAAAGCTCGAGCTGGTCAAGAAATTAGCATTCAGGTGTCCAAACCCTTCCCCTGCTG	1018
Db	838 TTTTTTTAAGTTACGGTCTGTGGAGAGAAATCAGCATCGAGGTCTCCAAACCCCTCTCTTACTG	897
QY	1019 GATCCGGATCANAGTCGCAGCTACTTTGGGGCTTTCAAGTTTCAGGACATAGACTGA	1075
Db	898 GATCCGGATCAGGATGCACATPACTTTGGGGCTTTTAAAGTTTCAGATATAGATTGA	954

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RESULT      4
US-08-584-031-2
; Sequence 2, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO. 2
; LENGTH: 1042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-584-031-2

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[illegible]

```

RESULT      5
US-08-780-496-2
; Sequence 2, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: AVI Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: single
TOPOLOGY: Linear
US-08-780-496-2

Query Match	2.7%	Score 58.4;	DB 5;	Length 1042;
Best Local Similarity	50.0%	Pred. No. 3.4e-05;		

Qy	713	AACATGACGTTAAAGCAACGGAAAACCTAAGGGTTAAACCAAGATGGCTTCATTACCTGTAC	772
Db	586	AAC TTGCAC TTGAGGAATGCTGAAC TGGT CATCCA TGA AAAAGGG TTTTAC TACATCAT	645
Qy	773	GCCAACATTTTCGCTTCGGGCATCAGAACAATCGGGAAGCGTACCCTACAGACTATCTTCAG	832
Db	646	TCCAAAACATACTTTCGATTTCAGGAGGAA-- --ATAAAAGAAAACACAAGAACGACAAA	702
Qy	833	CTGATGGTGCTATGCTGTTAAAAACCGACATCAAATCCCAGTTCTCATTAACCTGATGAAA	892
Db	703	C AAATGCTCAATATATATTTACAATACACAGTATTCCTCACCTATATGTTGATGAAA	762
Qy	893	GGAGGGAGCAGAAAAACTCGTCGGCAATCTCGAATCCACATTTTATTC CATAATGTT	952
Db	763	AGT GCTAGA AATAGTTGTTGGTCTAAGATGCGAATATGGACTCTATTCCCATCTATCAA	822
Qy	953	GGGGGATTTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGCCAACCTTCC	1013
Db	823	GGGGGATATTGAGCTTAGGAAAATGACAGATTTTTTGTCTCTGACAAATGAGCAC	882
Qy	1013	CTGCTGGATCCGGATCAAGATCGCAGCTACTTTGGGCGCTTCAAAGTT	1060
Db	883	TTGATACACATGGACCATGAAGCCAGTTTCTTTTCGCGGCGCTTTTTCAGTT	930

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RESULT      6
US-08-670-354-3
; Sequence 3, Application US/08670354
; Patent NO. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street

```

CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/670,154
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,168
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: HUAIC-dv
FEATURE:
NAME/KEY: CDS
LOCATION: 78..383
IS-08-670-354-3

Query Match 2.7%; Score 58.4; DB 2; Length 1521;
Best Local Similarity 50.0%; Pred. No. 4.1e-05;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

Qy	713	AACATGACGTATTAGCAACGGAAAACTAA·XGTTTACCAGAATGCCTTCTATTACCTGTAC	712
Db	425	AACTTCGACTTGAGGAATGGTGAACCTGGTCATCCATGAAAAGGGTTTTACTACATCAT	484
Qy	773	GCCAACAATTTGCTTTCCGGCATTGATAA·ATCCGGGAACCGTACCTACAGACTATCTTCAG	832
Db	485	TCCCAACATCACTTTCCGATTTTCAGAGG·VAAA--ATAAAGAAAAACACAAGAAGACGACAAA	541
Qy	833	CTGATGSGTAGTCGTTTAAACACAGCA·CAAATGCCAAGTCTCTCATACCTGATGAAA	892
Db	542	CAAATGGTCCATATATTTTACAAATACA·AAGTTATCTCGACCCCTATTTGTTGATGAAA	601
Qy	893	GGAGGAGCACGAAAACCTGGTCGGGCA·VTCTGAATCCCACCTTTTATCCATAAATGTT	952
Db	602	AGTGCTAGAAATAGTTGTGGTCTAAAG·ITGCAGANAATGGACTCTATTCCATCTATCAA	661
Qy	953	GGGGGATTTTTCAAAGTCGAGCTGGTG·VAGAAAATTAGCATTCAGGTGTCCAACCCCTCC	1012
Db	662	GGGGGAATTTTGAGCTTAAGGAAAATG·VCAGAAATTTTGTCTGTAAACAATAGCAC	721
Qy	1013	CTGCTGGATCCGGATCAGATCGGACGT·CTTTGGGGCTTTTCAAAGTT	1060
Db	722	TTCTAGACATGGACCATGAAGCCAGTT·TTTTCGGGGCTTTTATAGTT	769

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RESULT 7
PCT-US96-10895-3
: Sequence 3, Application PC/TUS9610895
: GENERAL INFORMATION:
: APPLICANT: Immunex Corporation.
: TITLE OF INVENTION: Cytokine That Induces Apoptosis
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple 7.5.2
: SOFTWARE: Microsoft Word, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/10895
: FILING DATE: 25-JUN-1996
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/496,632
: FILING DATE: 29-JUN-1995
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/548,368
: FILING DATE: 01-NOV-1995
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Anderson, Kathryn A.
: REGISTRATION NUMBER: 32,172
: REFERENCE/DOCKET NUMBER: 2835-WO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 233-0644
: TELEX: 756822
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1521 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: IMMEDIATE SOURCE:
: CLONE: HuAIC-dv
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 78..383
PCT-US96-10895-3

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	Query Match	2.7%	Score 58.4;	DB 6;	Length 1521;
	Best Local Similarity	50.0%;	Pred. No. 4.1e-05;		
	Matches 174;	Conservative 0;	Mismatches 171;	Indels 3;	Gaps
QY	713	AACATGACGTTAAGCACACGAAACAACTAAGGGTTTAAACCAAGATGGCTCTATTACCTGTAC	772		
Db	425	AACCTTGACATTGAGGAATGTGAACGTGTCATCCATGAAAAAGGGTTTTACTACATCTAT	484		
QY	773	GCCAAACATTTTGCCTTTCGGCATCATGAAACATCGGGAAGGCTACCTACACAGATATCTTCAG	832		
Db	485	TCCCAACACATACITTCGATTTTCAGGAGGAA--ATAAAGAAACACAAAGAACGCNAA	541		
QY	833	CTGATGTGTATGTCGTTAAACACGACATCAAAATCCCAAGTTTCATTAACCTGATGAAA	892		
Db	542	CAAAATGTCCAATATATTTTACAAATACACAAAGTTATCTCGACCTATATTGTTGATGAAA	601		

QY	893	CGAGGACGACGAAAACCTGGTCGGCGCAATCTCGAATCCCACTTTTATTTCCATAAATGTT	952
Db	602	AGTGCTAGAAAATAGTTGTTGGTCTAAAGATGCAGAAATATGGACTCTATTTCCATCTATCAA	661
QY	953	GGGGGATTTTTCAGCTCCGAGCTGGTGAAGAAATATAGCATTCAGGTGTCACACCTTCC	1012
Db	562	GGGGAATATTGAGCTTAAGAAATGACAGAAATTTTTTGTTCCTGTAACAATAGACAC	721
QY	1013	CTGCTGGATCGGATCAAGATCGGACGACTTTGGGGCTTTTCAAAAGTT	1060
Db	722	TTGATAGACATGGACCATGAAGCCAGTTTTCGGGGCCTTTTAGTT	769
RESULT 8			
US-08-670-354-1			
: Sequence 1, Application US/08670354			
: Patent No. 5763223			
: GENERAL INFORMATION:			
: APPLICANT: Steven R. Wiley and			
: APPLICANT: Raymond G. Goodwin.			
: TITLE OF INVENTION: Cytokine That Induces Apoptosis			
: NUMBER OF SEQUENCES: 9			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation			
: STREET: 51 University Street			
: CITY: Seattle			
: STATE: WA			
: COUNTRY: USA			
: ZIP: 98101			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: Apple Macintosh			
: OPERATING SYSTEM: Apple 7.5.2			
: SOFTWARE: Microsoft Word, Version 6.0.1			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/670,354			
: FILING DATE: 25-JUN-1996			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 08/496,632			
: FILING DATE: 29-JUN-1995			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 08/548,368			
: FILING DATE: 01-NOV-1995			
: CLASSIFICATION: 435			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Anderson, Kathryn A.			
: REGISTRATION NUMBER: 32,172			
: REFERENCE/DOCKET NUMBER: 2835-B			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: (206) 587-0430			
: TELEFAX: (206) 233-0644			
: TELEX: 756822			
: INFORMATION FOR SEQ ID NO: 1:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 1751 base pairs			
: TYPE: nucleic acid			
: STRANDEDNESS: single			
: TOPOLOGY: linear			
: MOLECULE TYPE: cDNA to mRNA			
: HYPOTHETICAL: NO			
: ANTI-SENSE: NO			
: IMMEDIATE SOURCE:			
: CLONE: huaIC			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: 88..933			
US-08-670-354-1			

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; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: huAIC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..933
; PCT-US96-10895-1

Query Match          2.7%; Score: 58.4; DB 6; Length 1751;
Best Local Similarity 50.0%; Pred No. 4.4e-05;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 713 AACATGACGTTAAGCAACGGAACAACTAAGTTTAAACCAAGATGGCTTCTATTACCTGTAC 772
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 583 AACTTCGCACTTGAGGAATGGTGAACCTGGTCAATCCATGAAAGGGTTTACTACATCTAT 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 773 GCCAACATTTGCTTTCCGGATCATGAATACATCGGGGAAGCGTACCTACAGACTATCTTCAG 832
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 643 TCCCAACATACATCTTCGATTTTCAGGAGGTA--ATAAAAGAAACACAAAGAACGACAAA 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 833 CTGATGCTGTATCTCGTTAAACCCACACATCAAAATCCCAAGTTCTCATACCTGATGAAA 892
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 CAATGGTCCATATATTTACAAATACAAAGTTATCTCGACCCCTATATTTGTTGATGAAA 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 893 GGAGGAGCAGCACGAAACAACTGGTGGGCA/TTCTGAATTCACACTTTTATTCCATAAATGTT 952
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 AGTGCTAGAAATAGTTTGGTCTAAG/TGCAGATATGGAGCTCATTTCCATCTATCAAA 819
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 953 GGGGGATTTTCAAGCTCCGAGCTGGTG/AGAAATTTAGCATTCAGGTGCCAACCCCTTCC 1012
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 GGGGGAATATTTGAGCTTAAGGAAATG/CAGAAATTTTGTCTCTCAACAAATGAGCAC 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1013 CTGCTGATCCGATCAAGATCCGAGTTCCTTTGGGGCTTTCAAAGTT 1060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 TTGATAGACATGGACCATGAAGCCAGTTTTCCTGGGGGCTTTTATAGTT 927
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-08-670-354-5
; Sequence 5, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,612
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,358
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: MUAIC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 47..919
; US-08-670-354-5

Query Match          2.5%; Score 54; DB 2; Length 1366;
Best Local Similarity 51.7%; Pred. No. 0.00046;
Matches 123; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 831 AGCTGATGGTGTATGTCTTAAACACCAGCATCAAAAATCCCAAGTTCTCATAACTGTATGA 890
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 687 AACAGCTGGTGCAGTACATCTACAAGTACACACGCTATCCGGATCCCATAGTGTCTCATGA 746
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 891 AAGGAGGGGACAGCAAAACTGGTGGGCAATTCGTAATTCACACTTTTATTCCATAAATG 950
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 747 AGAGCGCCACAGAAACAGCTGTGGTCCAGAGATGCCGAGTACGGACTGTACTCCATCTATC 806
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 951 TTGGGGGATTTTCAAGCTCCGAGCTGGTGAAGAAATTTAGCATTCAGTGTCCCAACCCCTT 1010
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 807 AGGAGGATTTTCGAGCTAAAAAATAATGACAGGATTTTGTCTGTGCAAAATGAAC 866
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1011 CCTGCTGGATCCGGATCAAGATCGCAGCTACTTTGGGGCTTTTCAAAAGTTTCAGGACAT 1068
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 867 ATTTGATGGACCTGGATCAAGAGCCAGCTTCTTTTGGAGCCTTTTAAATTAACATAAT 924
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
PCT-US96-10895-5
; Sequence 5, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:

```


GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2000, 09:56:08 ; Search time 1101.46 Seconds
(without alignments)
12298.703 Million cell updates/sec

Title: US-08-989-362-1
Perfect score: 2191
Sequence: 1 GCCAGGACCTCTGACCG.....TTTTGGTACTTAAAAATGCC 2191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues 14379728
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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6: gb_est6:*
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112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:

	Query Match	22.8%;	Score 499.4;	DB 35;	Length 514;
	Best Local Similarity	99.2%;	Pred. No. 1.1e-103;		
	Matches 511; Conservative	0;	Mismatches 3;	Indels 1;	Gaps
Qy	1503	GACCTGCAAAATAAGTCTTTTTTTCTAATGAGGAGAGAAAAATATATGTATTATTTTATATA	1562		
Db	1	GACCTGCAAAATAAGTCTTTTTTTCTAATGAGGAGAGAAAAATATATGTATTATTTTATATA	60		
Qy	1563	ATGCTTAAGTATATATTCAGGTGAATGTTTTCTGTGCAAAAGTTTTTGAAAATATATATTT	1622		
Db	61	ATGCTTAAGTATATATTCAGGTGAATGTTTTCTGTGCAAAAGTTTTTGAAAATATATATTT	120		
Qy	1623	GTGCTATAGTATTTTCATTCAAATAATTTAAAAATGCTCACGTGCACATATTTAATGTT	1682		
Db	121	GTGCTATAGTATTTTCATTCAAATAATTTAAAAATGCTCACGTGCACATATTTAATGTT	180		
Qy	1683	TTAATGTACAGATGATTTAACTGGTGCACHTTGTAAATCCCTCGAAGGTACTCGTAGC	1742		
Db	181	TAAATGTACAGATGATTTAACTGGTGCACHTTGTAAATCCCTCGAAGGTACTCGTAGC	240		
Qy	1743	TAAAGGGCGCAATACTGTGTTCTGTGGACCACATGTAGTTTTATTTCTTTATTTTTTTTAA	1802		

[illegible]

A0827122/C	A0827122	524 bp	DNA	GSS	27-AUG-1999
LOCUS	HS_5256_B2_C09_77A	RPCL-11	Human Male	BAC Library	Homo sapiens
DEFINITION	genomic clone Plate=832 Col=18 Row=F, DNA sequence.				
ACCESSION	A0827122				
VERSION	A0827122.1	GI:5793184			

KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 524)
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeong.med.buffalo.edu). Clones may be purchased from

Clones are derived from the human BAC library #11. For BAC library availability, please contact Pieter de Jong (pjeeter@dstong.med.buffalo.edu). Clones may be purchased from

Query Match 11.6%; Score 255.2; DB 28; Length 313;
Best Local Similarity 92.1%; Pred. No. 5.5e-48;
Matches 280; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 1885 AGGATGTTGGTCACCAAGTGGCTTTTCAAAATTTAGAGCTAATGACTTTTAGGAGCTGACA 1944
Db 1 AGGATGTTTTCACCAAGTGGCTTTTCAATTTTGAAGCTAATGACTTTTAGGAGCTGAGA 60
QY 1945 TAGCCAAAAGGATACATAATAGGCTACTGAAAATCTGTCAGGAGTATTTATGCAATAT 2004
Db 61 TACCCAAAAGGATACATAATAGGCTACTG-AAAATCTTTCAGGAGTATTTATGCAATAT 119
QY 2005 TGAACAGGTGCTTTTTTTTACAAGAGCTACAAATTTGTAATTTTGTCTTTTTTTTCCC 2064
Db 120 TGGACAGGTGCTTTTTTTTACAAGAGCTACAAATTTGTAATTTTGTCTTTTTTTTCCC 179
QY 2065 ATAGAAAATGTACTATAGTTTATCAGCCAAAACCAATCCACTTTTAAATTTAGTGAAG 2124
Db 180 ATAGAAAATTTACTATAGTTTATCAGCCAAAACCAATCCACTTTTAAATTTAGTGAAG 239
QY 2125 TTATTTTATTTACTGTACAAATAAAAGCATTTGTTCTGAATGGCATTTTGTGACTTAA 2184
Db 240 TTATTTTATTTACTGTACAAATAAAAGCATTTGTTCTGAATGTTAATTTTGGTACAAA 299
QY 2185 AAAT 2188
Db 300 AAAT 303

RESULT 5
A04117854
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

575 bp DNA GSS 23-MAR-1999
RPCI-11-185M9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-185M9,
DNA sequence.
A04117854
A04117854.1 GI:4475697
GSS.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: RPCI-11-185M9.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genet cs (http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html).
Seq primer: T7
Class: BAC end.
Location/Qualifiers
1. .575
/organism="Homo sapiens"
/db_xref="GDB:7570952"
/db_xref="taxon:9606"
/clone="RPCI-11-185M9"
/clone_lib="RPCI-11"
/sex="Male"

/cell_type="Lymphocytes"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"
BASE COUNT 178 a 79 c 120 g 198 t
ORIGIN

Query Match 11.6%; Score 254.2; DB 97; Length 575;
Best Local Similarity 77.9%; Pred. No. 1e-47;
Matches 403; Conservative 0; Mismatches 88; Indels 26; Gaps 7;

QY 1386 GGGTCTAACCCCTGACATGTGCCACTGGAACCTTGAATTAAGAGATGCCATCTCAT 1445
Db 79 GGGTGTGCTCCTGTCATGTCCTTCCGAGC-TGAAGTGAGAGGGGTGTCATCT-AG 136
QY 1446 TSCAAAGAAATGATAGTCTGAAGGGTTAAAGTTCTTTTGAATTTGTTACATTCGCTGGGAC 1505
Db 137 CGCAATGAAGGATCATCTGAAGGGGCAAAATCTTTTGAATTTGTTACATCATGCTGGAAC 196
QY 1506 CTGCAATAAGTCTTTTTTTTCTAATGAGGAGAGAAAATATATATGTTATTTATATAATG 1565
Db 197 CTGCAAAAAA---TACTTTTCTAATGAGGAGAG-AAAATATATGTTATTTATATAATA 252
QY 1566 TCTAAGTTATATTTTCAGGTGTAATGTTTCTGTCGCAAGTTTGTAAATATATTTTGTG 1625
Db 253 TCTAAGTTATATTTTCAGATGTAATGTTTCTTCTGCAAGTATTTGTAATTTATTTGTG 312
QY 1626 CTATAGTATTTGATTCAAAATATTTAAATATGTCACACGTTGACATATTTAATGTTTAA 1685
Db 313 CTATAGTATTTGATTCAAAATATTTAAATATGTCGCTGTTGACATATTTAATGTTTAA 372
QY 1686 AATGTACAGATGTAATTTAACTGGTGCACATTTGTAATTTCCCTG-----AAGGTACTCGTA 1740
Db 373 AATGTACAGACATATTTAACTGGTGCACATTTGTAATTTCCCTGGGAAACATTTGCAGCTA 432
QY 1741 GCTAAGGGGGCAGAAATATGTTTCTGGTGACCAATGATGTTATTTCTTTATCTTTT 1800
Db 433 AGGAGGGGGAAAAATGTTGTTTCTCTAATATCAAAATGCAATATTTCTTCATCTCTTTT 492
QY 1801 AACTTAATAGA-GTCTTCAGACTTGTCAAACATGTCAGCAAGCAAAATAAATAAATAAT 1859
Db 493 AAGTTAATAGATTTTTTTCAGACTTGTCAAAGCTGTGCTG-----AAAATAAT 538
QY 1860 AAAATGAATATCTTTGAATAAATAGTAGGATGTTGGTCT 1896
Db 539 AAAATGGATGCTTGAATAAATAGCAGGATGTTGGCC 575

RESULT 6
BB240334
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

306 bp mRNA EST 05-JUL-2000
BB240334 RIKEN full-length enriched, 3 days neonate thymus Mus
musculus cDNA clone A630081K02 3' similar to A6019048 Mus musculus
receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
mRNA sequence.
BB240334
BB240334.1 GI:8924942
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 306)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya
T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.


```

QY 2014 GTCTTTTTCACAGAGCTACAAATGTGTAATTTTGTCTCTTTTTCATAGAAAAT 2073
Db 123 TTCTTTTTCACAGAGCTACCAATGTGTAATTTTGTCTCTTTTTCATAGAAAAT 182
QY 2074 GTAATATAGTTTACAGCAAAACAA'CCACTTTTAAATTTAGTGAAGTTTATTTAT 2133
Db 183 GTAATATAGTTTACAGCAAAACAA'CCACTTTTAAATTTAGTGAAGTTTATTTAT 242
QY 2134 TATAGTACATAAAGCAATGTTTCTTAATGGCAATTTTGGTACTTAAAAAT 2188
Db 243 TATAGTACATAAAGCAATGTTTCTTAATTTTAAATTTTGGTACAAAAAT 297

RESULT 9
A0827168/c 529 bp DN1 GSS 27-AUG-1999
LOCUS HS 5256.B2.G09.T7A.RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate=832 Col.=18 Row=N, DNA sequence.
ACCESSION A0827168
VERSION A0827168.1 GI:5793230
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 529)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 832 row: N column: 18
Seq primer: 17
Class: BAC ends
High quality sequence stop: 529.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="Plate=832 Col=18 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT 147 a 121 c 102 g 153 t 6 others
ORIGIN

Query Match 10.5%; Score 229; DB 103; Length 529;
Best Local Similarity 72.9%; Pred. No. 5,7e-42;
Matches 336; Conservative 0; Mismatches 114; Indels 11; Gaps 3;

QY 864 AAATCCCAAGTTCTCATACCTGATGAAAGAGGGAGCAGCAAAACTGGTCGGCAATT 923
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Db 467 AAATCCCAAGTTCTCATACCTGATGAAGAGAGCAAGCAACCAAGATTTGGTCAGGGAATT 408
QY 924 CTGAATTCACATTTTATTTCCATAAATGTTGGGAGATTTTTCAGAGCTCCGAGCTGGTGAAG 983
||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 407 CTGAATTCACATTTTATTTCCATAAAGTTGGTGCATTTTGTAAAGTTAGGGTCTGGAGAGG 348
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QY 984 AAATTACATTCAGGTGTCCAAACCTTCCCTGCTGGATCCGGATCAAGATCCGAGCTACT 1043
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Db 347 AAATCAGCATCGAGGTCTCCAAACCTTCTTACTTGGATCCGGATCAGGATCAACATACT 288
||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
QY 1044 TTGGGGCTTTCAAGTTTCAGGACATAGACTAGACTCATTTTCGTGGACATATTAGCATGGA 1103
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Db 287 TTGGGGCTTTTAAAGTTTCGAGATATAGATTAGAGCCCGAGTTTTCGGAGTGT---ATGTA 231
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QY 1104 TGTCTTAGATGTTTGGAACTTCTTAAAAA-----ATGGATGATGCTTATACATGTGT 1156
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Db 230 TCTCTGGATGTTTGGAAACATTTTANACAGCCCAAGAAAGATGTATATAGGTGTGT 171
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QY 1157 AGACTACTAAGACATGCGCCACAGGTGTATGAAACTCACAGCCCTCTCTTTGAGCCT 1216
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QY 1217 GTACAGGTGTTGTATATGTTAAAGTCCATAGTGTATGTTAGATTCATGGTG-ATTACACAA 1275
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Db 110 GTAGAACACGAGTATTTACAGCCAGTGGGAGATGTTAGACTCATGCTGTGTTACACAA 51
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QY 1276 CGGTTTTCACAAATTTGTAATGATTTCCTTAAGAATTGAACCA 1316
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Db 50 TGGTTTGTAGATTNTGTAGNAGTACTAACGACTGCAACAA 10
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RESULT 10
BB216722 288 bp mRNA EST 30-JUN-2000
LOCUS BB216722 RIKEN full-length enriched, adult male aorta and vein Mus
DEFINITION musculus cDNA A530038L03 3' similar to AF019048 Mus musculus
receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
mRNA sequence.
ACCESSION BB216722
VERSION BB216722.1 GI:8881675
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 288)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
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Fax: +81-298-36-9098
Email: genome-res@tc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermotabilization and thermoactivation of thermolabile enzymes by

```

trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES	source
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location/Qualifiers
1. 288
  /organism="Mus musculus"
  /db_xref="taxon:10090"
  /clone="A530038L03"
  /clone_lib="RIKEN full-length enriched, adult male aorta
and vein"
  /sex="male"
  /tissue_type="aorta and vein"
  /dev_stage="adult"
  /lab_host="DH10B"
  /note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trihalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCGAGTTAATTAATTCCTCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

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BASE COUNT	96 a	42 c	42 g	108 t
ORIGIN				
Query Match		10.3%	Score 225.6;	DB 28;
Best Local Similarity		92.5%;	Pred. NO. 3.1e-41;	Length 288;
Matches 259;	Conservative	0;	Mismatches 19;	Indels 2;
				Gaps 2;

RESULT	11
BB236016	
LOCUS	
BB236016	314 bp mRNA EST
DEFINITION	BB236016 RIKEN full-length enriched, 3 days neonate thymus Mus
	05-JUL-2000

musculus cDNA clone A630056006 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BB236016.1 GI:8917884

EST. 1900

house mouse.

MUS MUSCULUS

Mus musculus: Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 314)

AUTHORS

.....

Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kadega, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shingawara, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Uetahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL

COMMENT

X-1000000

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URL: <http://genome.rtc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermoinactivation of the thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Katsunaga, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. *Genome Res.* 9 (3), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

source

1. 314
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/db_xref="taxon:10090"
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thymus"
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/dev_stage="3 days neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genetic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15',
GAGAGAGAGAGGATCCAGAGCCTTTTTTTTTTTTNN 3', cDNA was
prepared by using trhealose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapted of

sequence [5' GAGA:AGAGATTCTCGAGTTAATTAATAATCCCGCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

BASE COUNT 103 a 64 c 39 f 108 t
ORIGIN

Query Match 10.0%; Score: 219.8; DB 28; Length 314;
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Matches 261; Conservative 0; M.smatches 32; Indels 2; Gaps 2;

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QY 1955 GGATACATATAGGCTACTGAAATCTG'CAGGAGTATTTATGCAATTTATGAACAGGTG 2014

Db 63 GGATACATACAGGCTACTG-AAATCTC'CAGGAGCATTTATCCAAATTTATGAACAGGTG 121

QY 2015 TCCTTT-TTTTACAAGAGCTACAAATTTGT;AATTTTGTCTTTTTCCTCATAGAAAAAT 2073

Db 122 TCCTTTCTCCACAAGAGCTACAAATTTGT;AATTTTGTCTTTTTCCTCATAGGAAAT 181

QY 2074 GTACTATAGTTATCATGCCAAAAACAACACACTTTTAAATTTAGTGAAGTATTTTAT 2133

Db 182 GTACTATACCTATCATGCCAAAAACAACACACTTTTAAATTTAGTGAAGTATTTTAT 241

QY 2134 TATACGTACAAATAAAGAGATCTTCTCTCAATGCATTTTTCGTACTTAAAAAT 2188

Db 242 TATACGTACTATAAAGAGATCTCTCTCAATGTTAATTTTTCGTACTAAAAAAT 296

RESULT 12

BB229867

LOCUS

DEFINITION

BB229867 RIKEN full-length enriched, 3 days neonate thymus Mus
musculus cDNA clone A630024A04 3' similar to AF019048 Mus musculus
receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
mRNA sequence.

ACCESSION

BB229867

VERSION

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 282)

REFERENCE

AUTHORS

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota K., Kagawa I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Komio,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Miuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
Y., Shigenoto,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,K., Yasunishi,A., Yohota,T., Yoshida,K., Yoshiki,A., Yoshino
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno.H., et al.)

Unpublished (2000)

Contact: Yoshihide Hayashizaki

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Genome Science Laboratory

The Institute of Physical and Chemical Research (RIKEN), Genomic

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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

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URL:http://genome.rtc.riken.go.jp/

Carninci,P., Nishiyama,Y., vestlover,A., Itoh,M., Nagaoka,S., Sasaki

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N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
thermostabilization and thermoactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.
Location/Qualifiers
1..282

FEATURES

source

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A630024A04"
/clone_lib="RIKEN full-length enriched, 3 days neonate
thymus"
/tissue_type="thymus"
/dev_stage="3 days neonate"
/lab_host="DH10B"
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGAGTTAATTAATATCCCGCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

BASE COUNT 94 a 44 c 36 g 108 t

ORIGIN

Query Match 9.7%; Score 211.6; DB 28; Length 282;
Best Local Similarity 90.5%; Pred. No. 4.8e-38;
Matches 248; Conservative 0; Mismatches 24; Indels 2; Gaps 2;

QY 1915 TTAGAAGCTAATTGACCTTTAGGAGCTGCATAGCCAAAAGGATACATAATAGGCTACTG 1974

Db 1 TTTGAATCTAATTGAC-CTACGTCTGACATACCCCAAGGTTACATAATAGGCTACTG 59

QY 1975 AAAATCTGTCAGGAGTATTTATGCAATTTATGAACAGGTGCTTTTTTTTACAAGAGCTAC 2034

Db 60 AG-ATCTGTCAGGAGTATTTATGCAATTTATGAACAGGTCTCTTTTTTTACAAGAGCTAC 118

QY 2035 AAATTCGTAATTTTGTCTCTTTTTTTTCCCATAGAAATGTACTATAGTTTATCAGCCAA 2094

Db 119 AAATTCGTAATTTTGTCTCTTTTTTTTCCCATAGAAATGTACTATAGTTTATCAGCCAA 178

QY 2095 AAACAATCCACTTTTAAATTTAGTGAAGTATTTTATTTACTGTACAATAAAGCAT 2154

Db 179 AAACAATCCACTTTTAAATTTAGTGAAGTATTTTATTTACTGTACAATAAAGCAT 238

QY 2155 TGTCTCTGAATGCGATTTTGTGGTACTTAAAAAT 2188

Db 239 TGTCTCTGAATGCGATTTTGTGGTACTTAAAAAT 272

RESULT 13

BB234550

LOCUS

BB234550

277 bp

mRNA

EST

04-JUL-2000

DEFINITION	BB234550 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630049P08 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, mRNA sequence.
ACCESSION	BB234550
VERSION	BB234550.1
KEYWORDS	GI:8914405
SOURCE	mouse mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 277)
AUTHORS	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,K., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL	Unpublished (2000)
COMMENT	Contact: Yoshitide Hayashizaki Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: +81-298-36-9013 Fax: +81-298-36-9098 Email: genome-res@rtc.riken.go.jp, URL:http://genome.rtc.riken.go.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermostabilization and thermoactivation of the metabolizable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES	Location/Qualifiers 1..277 /organism="Mus musculus" /db_xref="taxon:10090" /clone="A630049P08" /clone_lib="RIKEN full-length enriched, 3 days neonate thymus" /tissue_type="thymus" /dev_stage="3 days neonate" /lab_host="DH10B" /note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15' GAGAGAGAAGGATCCAGAGCTCTTTTCTTTTCTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0 Second
SOURCE	

strand cDNA was prepared with the primer adapter of sequence [5' GAGAGGAGATTCTCGAGTTAAATTAATTCCTCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from lambda FLC I."					
BASE COUNT	96 a	49 c	30 g	102 t	
ORIGIN					
Query Match	9.2%; Score 200.6; DB 28; Length 277;				
Best Local Similarity	88.4%; Pred No. 1.5e-35;				
Matches 229; Conservative	0;	Mismatches 29;	Indels 1;	Gaps 1;	
QY 1930	CTTTAGGAGCTGACATAGGCCAAAAGAATACATAATAGGTACTGAAATCTGTCCAGGAG 1989				
Dbb					
Dbb 1	CTTCTGCACC CGAATACCCC AAAAGCATACATATTGGCTACTG-AAATCTATCAGGAC 59				
QY 1990	TATTATGCAATATTGAACAGGTGCTCTTTTTTACAAGAGCTCAAAATGTGAATTTTG 2049				
Dbb					
Dbb 60	TATTCATGCAATATTGAACAGCTGCTTTTTTTCACAAAGAGCTACAAATGTGAATTTTG 119				
QY 2050	TTTCTTTTTTTTCCCATAGAAAATGTACTAGTATTATCAGCCAAAAAACATCCACTTT 2109				
Dbb					
Dbb 120	TTTCTTTTTTTTCCCATAGAAAATGTACTAGTATTATCACC CAAAAACAAATCCACTTT 179				
QY 2110	TTAATTTAGTGAAGTTATTTTATTTATCTGTCAATAAAGCAATGTTCTCTGAATGGCA 2169				
Dbb					
Dbb 180	TTAATTTAGTGAAGTTATTTTATTTATCTGTCAATAAAGCAATTTTCTCTGAATGCTTA 239				
QY 2170	TTTTTTGGTACTTAAAAAT 2188				
Dbb					
Dbb 240	ATTTTGGTACAAAAAT 258				
RESULT 14					
BB236026					
LOCUS	BB236026	316 bp	mRNA	EST	04-JUL-2000
DEFINITION	Musculus cDNA clone A630056P12 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, mRNA sequence.				
ACCESSION	BB236026				
VERSION	BB236026.1 GI:8915651				
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 316)				
AUTHORS	Konno,H., Akizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci, K., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata, Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sugabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya, T., Tsunoda,Y., Watabiki,A., Wetanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino, M., Muramatsu.M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Konno,H., et al.)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Yoshihide Hayashizaki Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: +81-298-36-9013 Fax: +81-298-36-9098 Email: genome-res@rtc.riken.go.jp/ URL:http://genome.rtc.riken.go.jp/				

strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTCGAGTTAATTAAATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI."

BASE COUNT 84 a 35 c 31 g 101 t
ORIGIN

Query Match 8.6%; Score 187.4; DB 17; Length 251;
Best Local Similarity 92.5%; Pred. No. 1.6e-32;
Matches 197; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 1976 AAATCTGTCAGGAGTATTTATGCAATATTGAACAGGTGCTTTTTCACAGAGCTACA 2035
Db 20 AAATCTGTCAGGAGTATTTATCGACTATTGAACAGGTATCTTTTTCACAGAGCTACA 79
QY 2036 AATTGTAAATTTTGTCTCTTTTTCCTCCCATAGAAAATGTACTATAGTTTATCAGCCAAA 2095
Db 80 AATTGTAAATTTTGTCTCTTTTTCCTCCCATAGAAAATGTACTATAGTTTATCAGCCAAA 139
QY 2096 AAACATCCACTTTTAAATTTAGTGAAGTTATTATTACTGTACATAAAAGCATT 2155
Db 140 AAACATCCACTTTTAAATTTTGTGAAGTTATTATTACTGTACATAAAAGCATT 199
QY 2156 GTTCTGTAATGGCATTTTGTGTTACTTAAAAAT 2188
Db 200 TTTTCTGAATGTTAATTTTGTGTTACTTAAAAAT 232

Search completed: December 28, 2000, 18:03:43
Job time: 29255 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 28, 2000, 18:03:46 ; Search time 61.2 Seconds
(without alignments)
176.556 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYKLRSEEMGS.....LLDPDQDATYGFAPKVVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36.*
1: /cgn2_2/gcgdata/geneseq/geneseq/AA1980.DAT.*
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18: /cgn2_2/gcgdata/geneseq/geneseq/AA1997.DAT.*
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20: /cgn2_2/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /cgn2_2/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	19 W83194	Human osteoprotegerin
2	1675	100.0	316	19 W83017	Osteoclastogenesis
3	1675	100.0	316	19 W59654	Amino acid sequenc
4	1675	100.0	316	20 Y17874	Murine TRANCE. Mu
5	1675	100.0	316	21 Y84418	Amino acid sequenc
6	1675	100.0	316	21 Y84419	Amino acid sequenc
7	1554	92.8	294	19 W69956	NF-kB receptor act
8	1554	92.8	294	19 W68292	NF-kB receptor act
9	1417.5	84.6	317	19 W83195	Human osteoprotege
10	1417.5	84.6	317	19 W69957	NF-kB receptor act
11	1417.5	84.6	317	19 W68293	NF-kB receptor act
12	1417.5	84.6	317	21 Y84417	Amino acid sequenc

13	1409.5	84.1	317	19 W83018	Osteoclastogenesis
14	1297	77.4	244	19 W83019	A murine OCIF-bind
15	1107	66.1	246	19 W83020	Osteoclastogenesis
16	1101	65.7	245	20 Y17873	Human TRANCE. Hom
17	852	50.9	173	21 Y84421	Amino acid sequenc
18	852	50.9	187	21 Y84420	Amino acid sequenc
19	842	50.3	173	21 Y84422	A murine osteoprot
20	804.5	48.0	188	21 Y84423	An osteoprotegerin
21	794.5	47.4	182	21 Y84424	An osteoprotegerin
22	771	46.0	173	21 Y84425	DNA encoding osteo
23	732	43.7	173	21 Y84426	An osteoprotegerin
24	259.5	15.5	281	20 Y27016	Human Apo-2 ligand
25	259.5	15.5	281	20 Y27017	Human Apo-2 ligand
26	258.5	15.4	279	19 W76332	Human TL2 (TRAIL),
27	258.5	15.4	279	20 W95032	Tumour necrosis fa
28	258.5	15.4	281	18 W27134	Human Apoptosis in
29	258.5	15.4	281	18 W19787	Human Apoptosis in
30	258.5	15.4	281	18 W19777	Novel cytokine Apo
31	258.5	15.4	281	19 W76829	Human TL2 protein.
32	258.5	15.4	281	19 W56760	Human TRAIL polype
33	258.5	15.4	281	19 W44354	Human AGP-1. Homo
34	258.5	15.4	281	20 Y27012	Human Apo-2 ligand
35	258.5	15.4	281	20 Y01517	Protein associated
36	258.5	15.4	281	21 Y81956	Human Apo-2 ligand
37	252.5	15.1	281	20 Y27019	Human Apo-2 ligand
38	251.5	15.0	281	20 Y01516	Protein associated
39	250.5	15.0	281	20 Y27018	Human Apo-2 ligand
40	244	14.6	291	18 W19788	Mouse apoptosis in
41	244	14.6	291	19 W56762	Murine TRAIL polyp
42	244	14.6	291	19 W44353	Murine AGP-1. Mus
43	183	10.9	278	16 R79095	Rat Fas ligand enc
44	183	10.9	278	20 W98069	Rat Fas ligand (fa
45	183	10.9	278	20 W95040	Rat FasL protein.

ALIGNMENTS

RESULT 1

W83194
ID W83194 standard; Protein; 316 AA.

XX W83194;

XX 11-FEB-1999 (first entry)

XX Human osteoprotegerin binding protein from the 32D-F3 ins.

DE Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW hypercalcaemia; osteoclast differentiation and activation and activation receptor;
KW Paget's disease.

XX Homo sapiens.

XX WO9846751-A1.

XX 22-OCT-1998.

XX 15-APR-1998; 98WO-US07584.

XX 30-MAR-1998; 98US-0052521.

XX 16-APR-1997; 97US-0842842.

XX 23-JUN-1997; 97US-0880855.

XX (AMGE-) AMGEN INC.

XX Boyle WJ;

XX WPI; 1998-594578/50.

XX N-PSDB; W70284.

XX Nucleic acid encoding osteoprotegerin binding protein - useful for,

PT e.g. treating bone diseases by modulating osteoclast differentiation
PT and for diagnosis
XX
XX
XX Claim 19; Fig 1; 47pp; English.
XX
CC The present sequence is human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC osteoprotegerin (OG) in biological samples; to screen for specific
CC binding agents (particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (OPAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
XX
XX Sequence 316 AA;
XX
Query Match 100.0%; Score 1675; DB 19; Length 316;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYGYKYLRSSEMGSGVPHEG: LHPAPSAPAPAPPAAASRMFLALLGLGLGQ 60
Db 1 mrrasrdygykylrssemgsgvpheg: lhpapsapapappaaasrmflallglglgq 60
QY 61 VVCSIALFLYFRAQMDPNRISEDSTHCF: RLRLHENAGLQDSTLESDTLPSDCRRMKQ 120
Db 61 vvcsialflyfraqmdpnrisedsthcf: rlrlrhenagldstlesedtlpdsccrmkq 120
QY 121 AFOGAVOKELQHVIGVQRFSGAPAMMEG: WLDVAQRKPEAQPFALHTINAASIPSGSHK 180
Db 121 afggavqkelqhvigvqrfsgapammeg: wldvaqrgkpeaqpfahltinaasipsgshk 180
QY 181 VTLSWYHGRGWAKISNMTLSNCKLRVN: DGFYLYANICFRHHETSGSVPTDYLOLMVY 240
Db 181 vtlswwyhdrgwakisnmtlsngklrvn: idgfyllyanicfrhhetsgsvptdylolmvy 240
QY 241 VVKTSIKIPSSHNLKMGSGTKNWSGNSF: HFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Db 241 vvktstikipsshnlkmgsgtknwsngnsf: hfysinvvggffklrageeisiqvsnpslldp 300
QY 301 DQDATYFGAFKVQDID 316
Db 301 dqdatyfgafkvqdid 316
RESULT 2
ID W83017 standard; Protein: 316 AA.
XX
XX W83017;
XX
XX
DT 10-FEB-1999 (first entry)
XX
DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
XX
KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW osteoclast; bone absorption factor; bone disorder; calcium metabolism.
XX Unidentified.
XX
PN W09846644-AL.

XX
PD 22-OCT-1998.
XX
XX 15-APR-1998; 98WO-JP01728.
XX
PR 02-DEC-1997; 97JP-0332241.
PR 15-APR-1997; 97JP-0097808.
PR 09-JUN-1997; 97JP-0151434.
PR 12-AUG-1997; 97JP-0217897.
PR 21-AUG-1997; 97JP-0224803.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
XX Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
XX Washida N, Yamaguchi K, Yano K, Yasuda H;
XX WPI: 1998-594563/50.
DR N-PSDB: V69886.
XX
PT Protein binding to osteoclastogenesis inhibitory factor - useful
PT for, e.g. treatment and investigation of disorders of bone and
PT calcium metabolism
XX
PS Claim 8; Pages 106-108; 151pp; Japanese.
XX
CC The present sequence represents an osteoclastogenesis inhibitory factor
CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC separation and maturation of osteoclasts in the presence of bone
CC absorption factors such as calcitriol or parathyroid hormone (PTH).
CC OBM is isolated from stroma cells cultured in the presence of a bone
CC absorption factor by separation and solubilisation of membrane proteins
CC then affinity chromatography using OCIF. It exists in a full-sequence
CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
CC used for screening potential inhibitors and modifiers of its biological
CC activity, and screening for receptors to OBM which mediate its function.
CC These substances can then be used in the treatment of disorders of bone
CC function and calcium metabolism. The antibodies can be used for assay
CC of the protein, for investigative and diagnostic purposes, and as
CC components of drugs.
XX
XX Sequence 316 AA;
XX
Query Match 100.0%; Score 1675; DB 19; Length 316;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYGYKYLRSSEMGSGVPHEG: LHPAPSAPAPAPPAAASRMFLALLGLGLGQ 60
Db 1 mrrasrdygykylrssemgsgvpheg: lhpapsapapappaaasrmflallglglgq 60
QY 61 VVCSIALFLYFRAQMDPNRISEDSTHCF: RLRLHENAGLQDSTLESDTLPSDCRRMKQ 120
Db 61 vvcsialflyfraqmdpnrisedsthcf: rlrlrhenagldstlesedtlpdsccrmkq 120
QY 121 AFOGAVOKELQHVIGVQRFSGAPAMMEG: WLDVAQRKPEAQPFALHTINAASIPSGSHK 180
Db 121 afggavqkelqhvigvqrfsgapammeg: wldvaqrgkpeaqpfahltinaasipsgshk 180
QY 181 VTLSWYHGRGWAKISNMTLSNCKLRVN: DGFYLYANICFRHHETSGSVPTDYLOLMVY 240
Db 181 vtlswwyhdrgwakisnmtlsngklrvn: idgfyllyanicfrhhetsgsvptdylolmvy 240
QY 241 VVKTSIKIPSSHNLKMGSGTKNWSGNSF: HFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Db 241 vvktstikipsshnlkmgsgtknwsngnsf: hfysinvvggffklrageeisiqvsnpslldp 300
QY 301 DQDATYFGAFKVQDID 316
Db 301 dqdatyfgafkvqdid 316

```

RESULT 3
ID W59654 standard; Protein; 316 AA.
XX AC W59654;
XX 24-SEP-1998 (first entry)
XX DE Amino acid sequence of mouse 499E9 protein.
XX KW Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
XX KW antagonist; autoimmune disorder; rheumatoid arthritis;
XX KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
XX KW acute inflammatory response; antibody; antigen; cancer.
XX OS Mus sp.
XX Key Location/Qualifiers
XX FT Domain 1..49
XX FT /note= "intracellular domain"
XX FT Domain 70..316
XX FT /note= "extracellular domain"
XX PN WO9825958-A2.
XX PD 18-JUN-1998.
XX PF 12-DEC-1997; 97WO-US22766.
XX PR 13-DEC-1996; 96US-0032846.
XX PA (SCHE ) SCHERING CORP.
XX PI Gorman DM, Mattson JD;
XX PI
XX DR WPI; 1998-348452/30.
XX DR N-PSDB; V41489.
XX PT Mouse cell surface antigen, 499E9 protein - used to treat conditions
XX PT associated with abnormal physiology or development
XX PS Claim 1; Pages 8-11; 59pp; English.
XX CC This is the amino acid sequence of the mouse 499E9 protein, used
XX CC in the method of the invention to treat conditions associated with
XX CC abnormal physiology or development. The 499E9 protein is expressed
XX CC highly on polarised Th1 T cells. Binding of 499E9 to its receptor may
XX CC result in either immune cell expansion or apoptosis. Antagonists of
XX CC 499E9 may be used to modulate immune responses in abnormal situations,
XX CC e.g. autoimmune disorders including rheumatoid arthritis, systemic
XX CC lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
XX CC acute inflammatory responses in which T-cell expansion, activation or
XX CC immunological T-cell memory play an important role. The antibodies
XX CC can be used to raise anti-idiotypic antibodies which will be useful
XX CC in detecting or diagnosing various immunological conditions related to
XX CC the expression of antigens of 499E9. The antibodies, and fragments of
XX CC 499E9 can be used in the treatment of conditions associated with
XX CC abnormal physiology or development, including abnormal proliferation
XX CC (e.g. cancerous conditions) or degenerative conditions.
XX SQ Sequence 316 AA;

Query Match 100.0%; Score 1675; DB 19; Length 316;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYGYLRSSEPMGSGVPHPEGPLHPAPSAPAPPPAASRSMFLALGLGQ 60
DB 1 mrrasrdygykylrsseemsgvphpegplhpapsapapppaasrsmflalglgq 60
QY 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLQDSTLESDDLPSDCRMKQ 120
|||||

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Db 61 vvczialflyfraqmdpnrisdsthcfyrlrlhenagldstlesedtlpdsccrmkq 120
QY 121 AFQGAIVKELQHIYGPQRFSGAPAMMEGSLDVAQRGKPEAQPFAHLTTNAASIPSGSHK 180
|||||
Db 121 afqgavqkelghivgqrfsgapammegslvdaqrgkpeaqpfahltnaasipsghk 180
XX 181 VTLSSWYHDRGWAKISNMWTLNGLRVNODGFYLYANICF8HHETSGSVPTDYLOLMVY 240
|||||
Db 181 vtlsswyhdrgwaklsnmtlslngklrvnqdgfylyanlcf8hhetsgsvptdylolmvy 240
QY 241 VVKTSIKIPSSHNLKMGSTKNWGNSEPHFYSINVGGFFKLRAGEEISIQVSNP5LLDP 300
|||||
Db 241 vvktsikipssnlmkggstknwgnsephfysinvggffklrageeisqvsnp5lldp 300
QY 301 DQDATYFGAFKVDID 316
Db 301 dqdatyfgafkvqdid 316

RESULT 4
Y17874
ID Y17874 standard; Protein; 316 AA.
XX AC Y17874;
XX DT 17-AUG-1999 (first entry)
XX DE Murine TRANCE.
XX KW TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
XX KW TNF-related activation induced cytokine; immune response; cancer;
XX KW autoimmune disease; HIV; hypersensitivity; allergen.
XX OS Mus musculus.
XX PN WO9929865-A2.
XX PD 17-JUN-1999.
XX PF 14-DEC-1998; 98WO-US26486.
XX PR 11-DEC-1998; 98US-0989479.
XX PR 12-DEC-1997; 97US-0989479.
XX PR 03-MAR-1998; 98US-0034099.
XX PA (UVRQ ) UNIV ROCKEFELLER.
XX PI Choi Y, Josien R, Steinman R, Won B;
XX DR WPI; 1999-385609/32.
XX DR N-PSDB; X80224.
XX PT TNF like proteins for treating autoimmunity and cancer
XX PS Claim 9; Fig 3; 164pp; English.
XX CC The present sequence represents murine TNF-related activation induced
XX CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX CC variants, fragments, derivatives or analogues may be used as modulators
XX CC of immune response in a mammal comprising, antisense sequences to
XX CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX CC Agonists and antagonists of TRANCE, can be used to modulate immune
XX CC response by increasing or decreasing the life span of mature dendritic
XX CC cells and increasing or decreasing T cell activation. These techniques
XX CC are especially useful for treating immune system related conditions such
XX CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
XX CC The TRANCE polypeptides can be used to increase the viability of
XX CC dendritic cells in vivo or in vitro, especially when used in conjunction
XX CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
XX CC CD40L or TNF-alpha).
XX SQ Sequence 316 AA;

```

Query Match	100.0%;	Score 1675;	DB 20;	Length 316;
Best Local Similarity	100.0%;	Pred. No. 6.4e-144;		
Matches 316;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MRRASRDYGYKYLRSSEMGSGVPHGEG'LHPAPAPAPAPPPAASRSMFLALLGLGLGQ	60	
DB	1	mrrasrdygykylrsseemsgsgvphgglhlpasapapppaasrsmflallglglgq	60	
QY	61	VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLQDSTLESDYLPDSCRRMKQ	120	
DB	61	vvcsialflyfraqmdpnrisdsthcfyriilrlhenagldstlesedtlpdsccrmkq	120	
QY	121	AFQGAQVQKELQHVGPQRFSGAPAMMEG:WLDVAQKQKPEAPFAHLLTNAASIPSGSHK	180	
DB	121	afqgavqkelqhvpgprfsgapammeg:wladvagrkgpeaqpfahltinaasipsgshk	180	
QY	181	VTLSSWYHHRGWAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLQVMY	240	
DB	181	vtlsswyhhrgwakismnltlsngklrvn:dgfylyanicfrhhetsgsvptdyqlqvmv	240	
QY	241	VVKTSLKIPSSHNLKMGSTKNWGNSEIHFYSINVGFFKLRAGEEISIQVSNPSLLDP	300	
DB	241	vvktsikipsshnlmkgstknwgnseihfysinvvgffklrageeisiqvsnpslldp	300	
QY	301	DQDATYFGAFKVDID 316		
DB	301	dqdatyfgafkvqdid 316		
RESULT	5			
Y84418				
ID	Y84418	standard; Protein; 316 AA.		
XX	AC	Y84418;		
XX	AC			
XX	DT	25-JUL-2000 (first entry)		
XX	DE	Amino acid sequence of a murine osteoprotegerin ligand (OPGL).		
XX	KW	Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;		
XX	KW	tumour necrosis factor receptor; type II transmembrane protein;		
XX	KW	osteoclast differentiation; CSF-1; osteoclast activator;		
XX	KW	immune response; osteoporosis; bone resorption.		
XX	OS	Mus musculus.		
XX	FH	Key	Location/Qualifiers	
XX	FT	Domain	48..71 "transmembrane domain"	
XX	FT	Domain	/note= "transmembrane domain"	
XX	FT	Domain	70..157	
XX	FT	Domain	/note= "extracellular stalk domain"	
XX	FT	Domain	152..316	
XX	FT	Region	/note= "tumour necrosis factor-like domain"	
XX	FT	Region	158..317	
XX	FT		/note= "active ligand moiety"	
XX	PN	WO200015807-A1.		
XX	PN			
XX	PD	23-MAR-2000.		
XX	PF	13-SEP-1999;	99WO-DK00481.	
XX	PR	15-SEP-1998;	98DK-0001164.	
XX	PR	02-OCT-1998;	98US-0102896.	
XX	PA	(MEBI-) M & E BIOTECH AS.		
XX	PI	Halkier T, Haaning J;		
XX	DR	WPI; 2000-271444/23.		
XX	DR	N-PSDB; 299965.		
XX	XX			

PT	In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used			
PT	to treat, prevent and ameliorate osteoporosis -			
XX	PS	Claim 17; Page 81-82; 110pp; English.		
XX	CC	The present sequence represents a murine osteoprotegerin ligand (OPGL).		
XX	CC	Osteoprotegerin is a secreted member of the tumour necrosis factor		
XX	CC	receptor family, which blocks osteoclastogenesis in a dose dependent		
XX	CC	manner. The OPGL protein is synthesised as a type II transmembrane		
XX	CC	protein. The murine and human OPGL polypeptides are 87% homologous, OPGL		
XX	CC	is a potent osteoclast differentiation factor when combined with CSF-1.		
XX	CC	It is not capable of inducing osteoclast differentiation in the absence		
XX	CC	of CSF-1. OPGL is also an activator of mature osteoclasts. The		
XX	CC	specification describes a method for the in vivo down-regulation of		
XX	CC	OPGL activity in an animal. The method comprises using at least one OPGL		
XX	CC	polypeptide or subsequence, and/or at least one OPGL analogue to induce		
XX	CC	an immune response in the animal. The method and OPGL polypeptide are		
XX	CC	useful for treating, preventing and ameliorating osteoporosis or other		
XX	CC	diseases or conditions characterised by excessive bone resorption.		
XX	CC			
SQ	Sequence	316 AA;		
Query Match	100.0%;	Score 1675;	DB 21;	Length 316;
Best Local Similarity	100.0%;	Pred. No. 6.4e-144;		
Matches 316;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MRRASRDYGYKYLRSSEMGSGVPHGEG'PLHPAPAPAPAPPPAASRSMFLALLGLGLGQ	60	
DB	1	mrrasrdygykylrsseemsgsgvphgplhlpasapapppaasrsmflallglglgq	60	
QY	61	VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQ	120	
DB	61	vvcsialflyfraqmdpnrisdsthcfyriilrlhenagldstlesedtlpdsccrmkq	120	
QY	121	AFQGAQVQKELQHVGPQRFSGAPAMMEG:WLDVAQKQKPEAPFAHLLTNAASIPSGSHK	180	
DB	121	afqgavqkelqhvpgprfsgapammeg:wladvagrkgpeaqpfahltinaasipsgshk	180	
QY	181	VTLSSWYHHRGWAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLQVMY	240	
DB	181	vtlsswyhhrgwakismnltlsngklrvn:dgfylyanicfrhhetsgsvptdyqlqvmv	240	
QY	241	VVKTSLKIPSSHNLKMGSTKNWGNSEIHFYSINVGFFKLRAGEEISIQVSNPSLLDP	300	
DB	241	vvktsikipsshnlmkgstknwgnseihfysinvvgffklrageeisiqvsnpslldp	300	
QY	301	DQDATYFGAFKVDID 316		
DB	301	dqdatyfgafkvqdid 316		
RESULT	6			
Y84419				
ID	Y84419	standard; Protein; 316 AA.		
XX	AC	Y84419;		
XX	AC			
XX	DT	25-JUL-2000 (first entry)		
XX	DE	Amino acid sequence of a murine osteoprotegerin ligand (OPGL).		
XX	KW	Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;		
XX	KW	tumour necrosis factor receptor; type II transmembrane protein;		
XX	KW	osteoclast differentiation; CSF-1; osteoclast activator;		
XX	KW	immune response; osteoporosis; bone resorption.		
XX	OS	Mus musculus.		
XX	FH	Key	Location/Qualifiers	
XX	FT	Region	49..69	
XX	FT	Domain	/note= "transmembrane region"	
XX	FT	Domain	70..157	

QY 143 PAMWESWLDVAORGRPEAOPFAHLTINLASIPSGSHKVTLSWYHDSRGWAKISNMTLSN 202
 Db 121 pammegswldvaqrgrpeaopfahtin:asipsgshkvtlsswyhdsrgwaksnmtlsn 180
 QY 203 GKLRVNDGFFYYLYANICFRHETSGSVTDYQLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
 Db 181 gklrvnqdgffyylyanicfrhetskvsytdylqlmvyvvtksik:ipsshnlmkggstkn 240
 QY 263 WSGNSEFHYFINVGGFFKLRAAGEEISIQVSNPSSLDPDQDATYFGAFKVDID 316
 Db 241 wsgnsefhfysinvggffklrageeisi:qvsnpslldpqdqatyfgafkvqdid 294

RESULT 8

W68292
 ID W68292 standard; Protein: 294 AA.

AC W68292;

XX 08-OCT-1998 (first entry)

DE NF-kB receptor activator RANK ligand (RANKL).

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.

XX Mus musculus.

XX W09828424-A2.

PD 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23866.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

XX (IMM) IMMUNEX CORP.

PI Anderson DM, Galibert LJ, Marashovsky E;

XX WPI: 1998-377655/32.

DR N-PSDB; V41371.

XX New isolated receptor activator of necrosis factor-kappa B - useful
 PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis

XX Example 7: Pages 55-57; 80pp; English.

XX This represents a murine RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 294 AA;

Query Match 92.8%; Score 1554; DB 19; Length 294;

50 55"

Best Local Similarity 99.7%; Pred. No. 5.3e-133;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 23 GVPEHGPLHPAPAPAPPPAASRSMLALLGLGLGVVCSIALFLYFRAQMDPNRISE 82
 Db 1 gvpehGPLHPAPAPPPAASRSMLALLGLGLGVVCSIALFLYFRAQMDPNRISE 60
 QY 83 DSTHCFYRILRLHENAGLQDSTLSEDTLPDSRRMKQAFQAVOKELQHTIVGQRFSGA 142
 Db 61 dsthcfyRILRLhenadlqdstlesedtlpdsrrmkqafqgavqkelqhlvggqrfsga 120
 QY 143 PAMWESWLDVAORGRPEAOPFAHLTINAAISIPSGSHKVTLSWYHDSRGWAKISNMTLSN 202
 Db 121 pammegswldvaqrgrpeaopfahtlnaa:isipsgshkvtlsswyhdsrgwaksnmtlsn 180
 QY 203 GKLRVNDGFFYYLYANICFRHETSGSVTDYQLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
 Db 181 gklrvnqdgffyylyanicfrhetskvsytdylqlmvyvvtksik:ipsshnlmkggstkn 240
 QY 263 WSGNSEFHYFINVGGFFKLRAAGEEISIQVSNPSSLDPDQDATYFGAFKVDID 316
 Db 241 wsgnsefhfysinvggffklrageeisi:qvsnpslldpqdqatyfgafkvqdid 294

RESULT 9

W83195
 ID W83195 standard; Protein: 317 AA.

AC W83195;

XX 11-FEB-1999 (first entry)

DE Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.

XX Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODA;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 KW Paget's disease.

XX Homo sapiens.

XX W09846751-A1.

XX 22-OCT-1998.

XX 15-APR-1998; 98WO-US07584.

XX 30-MAR-1998; 98US-0052521.

PR 16-APR-1997; 97US-0842842.

PR 23-JUN-1997; 97US-0880855.

XX (AMGE-) AMGEN INC.

XX Boyle WJ;

XX WPI: 1998-594578/50.

DR N-PSDB; V70285.

XX Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis

XX Claim 19; Fig 4; 47pp; English.

XX The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OPG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation

KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF.
 XX

OS Homo sapiens.

PN WO9828424-A2.

PD 02-JUL-1998.

PF 22-DEC-1997; 97WO-US23866.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

XX (IMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Marasovsky E;

PI WPI: 1998-377655/32.

DR N-PSDB; V41372.

XX New isolated receptor activator of necrosis factor-kappa B - useful
 PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis
 PT

PS Example 7; Pages 59-60; 80pp; English.

XX This represents a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 317 AA;

Query Match 84.6%; Score 1417.5; DB 19; Length 317;
 Best Local Similarity 84.3%; Pred. No. 1.3e-120;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYKLRSEEMSGPGVPHG;LHPAPSAAPAPPAAASRSMFLALLGLGLGQ 60

DB 1 mrrasrdykyrgseemsgpggphg;ph-appphqppaaasrmfvaliglgq 59

QY 61 VVCSIALFLYFRAQMDPNRISEDSHCF;RIILRLHENAGLQSTLSEDT--LPDSCRRM 118

DB 60 vvcsvalfyfraqmdpnriisedgthci;riilrlhenadfqdtlesqdklipdscrr 119

QY 119 KQAFQCAVQKELQHIIVGPFQSCAPAMM;GSLWLDVAQKGPKEAPQPAHLTINAAIPSGS 178

DB 120 kqafgavqkqlhivgsgnhiaraekamvigswldiakrskleaqpfahitnatdipsgs 179

QY 179 HKVTLSSWYHWRGAKISNMNLTSLNGKL;NODGFYLYANICFRHETSGSVPTDYLOLM 238

DB 180 hkvslsswyhwrwakismntsfngkli;nqdgfylyanicfrhnetsgdlateylqlm 239

QY 239 VYVTKTSIKIPSSHNLKMGSTKNWSGN;EEHFYSYINVGGFFKLRAGEETISQVSNPSLL 298

DB 240 vvytktsikipshtlmkgstkysgmnefhfysinvvgffklrsggeelievsnpsll 299

QY 299 DPDDATYFCAFKVQDID 316

|||||

DB 300 dpdqdyfgafkvrddid 317

RESULT 12

Y84417

ID Y84417 standard; Protein; 317 AA.

XX Y84417;

XX 25-JUL-2000 (first entry)

XX Amino acid sequence of a human osteoprotegerin ligand (OPGL).

XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 49..69

FT /note= "transmembrane region"

FT Domain 70..157

FT /note= "extracellular stalk domain"

FT Region 158..317

FT /note= "active ligand moiety"

XX WO200015807-A1.

XX 23-MAR-2000.

XX 13-SEP-1999; 99WO-DK00481.

XX 15-SEP-1998; 98DK-0001164.

XX 02-OCT-1998; 98US-0102896.

XX (MEBT-) M & E BIOTECH AS.

XX Halkier T, Haaning J;

XX WPI: 2000-271444/23.

XX N-PSDB; Z99964.

XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT to treat, prevent and ameliorate osteoporosis -
 PT

PS Claim 19; Page 78-79; 110pp; English.

XX The present sequence represents a human osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.

XX Sequence 317 AA;

Query Match 84.6%; Score 1417.5; DB 21; Length 317;

Best Local Similarity 84.3%; Pred. No. 1.3e-120;

Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYKLRSEEMSGPGVPHG;LHPAPSAAPAPPAAASRSMFLALLGLGLGQ 60

|||||

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 28, 2000, 18:48:36 ; Search time 157.95 Seconds
(without alignments)
33.533 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYKLSRSEMGs.....LLDPQDATYGFVKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6CTUS_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	2	US-08-842-842-7
2	1554	92.8	294	3	US-08-996-139-11
3	1417.5	84.6	317	3	US-08-996-139-13
4	258.5	15.4	281	1	US-08-670-354-2
5	258.5	15.4	281	3	US-08-584-031-1
6	258.5	15.4	281	3	US-08-780-496-1
7	258.5	15.4	281	4	PCT-US96-10895-2
8	244	14.6	291	1	US-08-670-354-6
9	244	14.6	291	1	PCT-US96-10895-6
10	173.5	10.4	281	2	US-08-810-453-2
11	173.5	10.4	281	3	US-08-815-190A-2
12	173.5	10.4	281	4	PCT-US95-00362-2
13	171.5	10.2	261	1	US-07-940-605A-2
14	171.5	10.2	261	1	US-08-184-422-8
15	171.5	10.2	261	1	US-08-360-923A-2
16	171.5	10.2	261	1	US-08-446-922-4
17	171.5	10.2	261	2	US-08-431-055-4
18	171.5	10.2	261	2	US-08-690-096-2
19	171.5	10.2	261	2	US-08-249-189-12
20	171.5	10.2	261	2	US-08-484-624A-12
21	171.5	10.2	261	2	US-08-477-733B-12
22	171.5	10.2	261	3	US-08-763-995-2
23	171.5	10.2	261	3	US-09-088-913A-12
24	171.5	10.2	261	3	US-08-589-771B-8
25	171.5	10.2	261	4	PCT-US93-10034-4
26	169	10.1	279	4	PCT-US95-00362-5
27	160	9.6	473	2	US-08-249-189-16
28	160	9.6	473	2	US-08-484-624A-16

29	160	9.6	473	2	US-08-477-733B-16	Sequence 16, Appl
30	160	9.6	473	3	US-09-088-913A-16	Sequence 16, Appl
31	159	9.5	273	1	US-08-446-922-11	Sequence 11, Appl
32	159	9.5	273	2	US-08-249-189-21	Sequence 21, Appl
33	159	9.5	273	2	US-08-484-624A-21	Sequence 21, Appl
34	159	9.5	273	2	US-08-477-733B-21	Sequence 21, Appl
35	159	9.5	273	3	US-09-088-913A-21	Sequence 21, Appl
36	157	9.4	260	1	US-08-446-922-6	Sequence 6, Appl
37	157	9.4	260	2	US-08-431-055-2	Sequence 2, Appl
38	157	9.4	260	2	US-08-249-189-2	Sequence 2, Appl
39	157	9.4	260	2	US-08-484-624A-2	Sequence 2, Appl
40	157	9.4	260	2	US-08-477-733B-2	Sequence 2, Appl
41	157	9.4	260	3	US-09-088-913A-2	Sequence 2, Appl
42	157	9.4	260	4	PCT-US93-10034-6	Sequence 6, Appl
43	154	9.2	151	1	US-07-940-605A-3	Sequence 3, Appl
44	154	9.2	151	2	US-08-690-096-3	Sequence 3, Appl
45	152	9.1	149	3	US-08-584-031-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-842-842-7
; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91230-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,842
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-842-7

Query Match 100.0%; Score 1675; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.2e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRRASRDYGYKLSRSEMGSGPGVPEHGLHPAPAPAPPPAASRSMFLALLGLGLGQ	60
DB	1	MRRASRDYGYKLSRSEMGSGPGVPEHGLHPAPAPAPPPAASRSMFLALLGLGLGQ	60
QY	61	VVCSTALFLYFRAQMDPNRISDSSTHCFYRIURLHLENAGLQDSTLESDTLPDSCRMKQ	120
DB	61	VVCSTALFLYFRAQMDPNRISDSSTHCFYRIURLHLENAGLQDSTLESDTLPDSCRMKQ	120
QY	121	AFQGAQVQKELQHVIGPQRFSGAPAMMEGSLDVAQKPKPAQFFAHLTINAAIPSGSHK	180
DB	121	AFQGAQVQKELQHVIGPQRFSGAPAMMEGSLDVAQKPKPAQFFAHLTINAAIPSGSHK	180

QY 181 VTLSWYHDRGWAKISNMTLSNCKLRVNJDGFYLYLANICFRHHETSGSVPTDYQLQVMY 240
Db 181 VTLSWYHDRGWAKISNMTLSNCKLRVNJDGFYLYLANICFRHHETSGSVPTDYQLQVMY 240
QY 241 VVKTSIKIPSSHNLMKGGSTKNWGSNSEHFYSINVGFFKLRAGEISIOVSNPSSLLDP 300
Db 241 VVKTSIKIPSSHNLMKGGSTKNWGSNSEHFYSINVGFFKLRAGEISIOVSNPSSLLDP 300
QY 301 DQDATYFGAFKVDID 316
Db 301 DQDATYFGAFKVDID 316
RESULT 2
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/06,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/81,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/77,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-11

Query Match 92.8%; Score: 1554; DB 3; Length 294;
Best Local Similarity 99.7%; Pred. No. 1.7e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GYPHEGLHPAPSAPAPAPPPAASRMFIALGLGLGVVCSIALFLYFRAQMDPNRISE 82
Db 1 GYPHEGLHPAPSAPAPAPPPAASRMFIALGLGLGVVCSIALFLYFRAQMDPNRISE 60

QY 83 DSTHCFYRILRLHENAGLDSTLESDTLDPSCRRMKQAFQAVOKELQHTVGPORFSGA 142
Db 61 DSTHCFYRILRLHENAGLDSTLESDTLDPSCRRMKQAFQAVOKELQHTVGPORFSGA 120
QY 143 PAMMEGSLWDAVQKGPFAHLTINAASIPSGSHKVTLSWYHDRGWAKISNMTLSN 202
Db 121 PAMMEGSLWDAVQKGPFAHLTINAASIPSGSHKVTLSWYHDRGWAKISNMTLSN 180
QY 203 GKLRVNDGFFYLYLANICFRHHETSGSVPTDYQLQVMYVVKTSIKIPSSHNLMKGGSTKN 262
Db 181 GKLRVNDGFFYLYLANICFRHHETSGSVPTDYQLQVMYVVKTSIKIPSSHNLMKGGSTKN 240
QY 263 WSGNSEHFYSINVGFFKLRAGEISIOVSNPSSLLDPDQDATYFGAFKVDID 316
Db 241 WSGNSEHFYSINVGFFKLRAGEISIOVSNPSSLLDPDQDATYFGAFKVDID 294
RESULT 3
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

Query Match 84.6%; Score 1417.5; DB 3; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.5e-132;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYKLRSEDMGSGPGVPHGLHPAPSAPAPPPAASRMFIALGLGLGQ 60

[illegible]

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RESULT      4
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Willey and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

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```

RESULT 5
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: prt
; ORGANISM: Homo sapiens
US-08-584-031-1

```

```

Query Match      15.4%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred. No. 9.8e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps

Qy 43 PAASRSMFLAALLGLGLQGVVCSTALFLYFRAQMD--PNRISDSHSTHCFFRIURLHENAGL 100
   | : : : : | : | : : : : | : : : : | : : : : |
Db 10 PSLGQTCVLIVFTVLQSLQCLVAVTVYFTNELKQMDKYSGIACF-----LKEDSDY 64
   | : : : : | : : : : | : : : : | : : : : |
Qy 101 QDSTLESEDTLPDSCRMKQAFQAGVOK-----ELQHIIVGPQRFSGAPAMM 146
   | : : : : | : : : : | : : : : | : : : : |
Db 65 WDP--NDEESMNSPCWQWQWLHOLVRKMKILRTSEETITVQEKQONISPL----- 113
   | : : : : | : : : : | : : : : | : : : : |
Qy 147 EGSMLDVAQKQKPEAOPFAHL-----INAAISPGSHKVTL-----SSWYHDR-GWAKIS 196
   | : : : : | : : : : | : : : : | : : : : |
Db 114 -----VREGQPQVRA--AHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165
   | : : : : | : : : : | : : : : | : : : : |
Qy 197 NMTLSNGKLKRVNODGFFYLVLVYANICFRHHETSGSVPTDYQLQWVYVVKTSIKIPSSHNLMK 256
   | : : : : | : : : : | : : : : | : : : : |
Db 166 NLHLRNGELVTHEKGFFYIYSQTYFRFQEEIKENTKNDKQMVQYIKVYT-SYDPDILLMK 224
   | : : : : | : : : : | : : : : | : : : : |
Qy 257 GGSTKKNWSGNSEPHFYSINVGGFKKLRAGEETISIQVNSPSSLDPDODATYFGAFKV 312
   | : : : : | : : : : | : : : : | : : : : |
Db 225 SARNSCWSKDAEYGLXISYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLV 280
   | : : : : | : : : : | : : : : | : : : : |

RESULT 6
US-08-780-496-1
; Sequence 1, Application US/08780496

```

```

; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Cnuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS;
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978v1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-780-496-1

```

```

Query Match      15.4%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred No. 9.8e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 43 PAASRSMFLALLGLGLGVVCSIALFLYRAQMD--PNRISEDSTHCFYRLRLHENAGL 100
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 10 PSLGQCVLVIIFTVLQSLCVAVTYVYTNELKQMDKYSGIACF-----LKEDDSY 64
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 101 QDSTLESEDTLDPDCRRMKQAFQGVOK -----ELQHVGPQRFSGAPAMM 146
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 65 WDP--NDEESMNSPCWQVWKQLRQLVRKMLRTSEETISTVQEKQONISPL----- 113
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 147 EGSWLDVAQRGKPEAQPFAPHLT-----IHAASIPSGSHKVTL-----SSWYHDR-GWAKIS 196
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 114 -----VREGRQORVA--AHITGRGRSHITLSSPNKNEKALGRKINSWESSRSGHSFELS 165
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 197 NMTLSNGLRVNODGFYYLYANICFRHHITSGSVPTDYQLQMLVYVVKTSIKIPSSHNLMK 256
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 166 NLHLRNGELVIEHKGFFYYISQTYFRQEEIKENTKNDKQWQVYIKYT--SYDPDILLMK 224
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 257 GGSTKNWSNSEFHFYSINVGFFKLRAKEEISQVSNPSLLDDPDQDATYFGAFKV 312
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 225 SARNSCWSKDAEYGLYSIQGGIFELKEDRIFVSVTNEHLIDMDHEASFFFGAFLV 280
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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RESULT 7
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895;
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle

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2. 73

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; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10895-2

```

```

Query Match      15.4%; Score 258.5; DB 4; Length 281;
Best Local Similarity 26.4%; Pred No. 9.8e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 43 PAASRSMFLALLGLGLGVVCSIALFLYRAQMD--PNRISEDSTHCFYRLRLHENAGL 100
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 10 PSLGQCVLVIIFTVLQSLCVAVTYVYTNELKQMDKYSGIACF-----LKEDDSY 64
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 101 QDSTLESEDTLDPDCRRMKQAFQGVOK -----ELQHVGPQRFSGAPAMM 146
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 65 WDP--NDEESMNSPCWQVWKQLRQLVRKMLRTSEETISTVQEKQONISPL----- 113
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 147 EGSWLDVAQRGKPEAQPFAPHLT-----IHAASIPSGSHKVTL-----SSWYHDR-GWAKIS 196
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 114 -----VREGRQORVA--AHITGRGRSHITLSSPNKNEKALGRKINSWESSRSGHSFELS 165
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 197 NMTLSNGLRVNODGFYYLYANICFRHHITSGSVPTDYQLQMLVYVVKTSIKIPSSHNLMK 256
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 166 NLHLRNGELVIEHKGFFYYISQTYFRQEEIKENTKNDKQWQVYIKYT--SYDPDILLMK 224
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 257 GGSTKNWSNSEFHFYSINVGFFKLRAKEEISQVSNPSLLDDPDQDATYFGAFKV 312
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 225 SARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFFGAFLV 280
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

```

RESULT 8
US-08-670-354-6
; Sequence 6, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

```


US-08-810-453-2
; Sequence 2, Application US/08810453
; Patent No. 5858990
; GENERAL INFORMATION:
; APPLICANT: Walsh, Kenneth
; TITLE OF INVENTION: FAS LIGAND COMPOSITIONS FOR TREATMENT OF
; PROLIFERATIVE DISORDERS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Jacks, P.C.
; STREET: Federal Reserve Plaza, 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,453
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: S1237,7004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)720-3500
; TELEFAX: (617)720-2441
; TELEX: 343
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-453-2

Query Match 10.4%; Score 173.5; DB 2; Length 281;
Best Local Similarity 21.2%; Pred. No. 2.4e-09;
Matches 67; Conservative 42; Mismatches 108; Indels 99; Gaps 9;
QY 22 PGVPHGGLHPAPSAPAPPPAASR-----SMFLALLGLGL 58
DB 40 PGQRRPPPPPPPPPPPPPPPLPLPLPLKKGHNHSTGCLLVMMFFVVLVALVGLGL 99
QY 59 GQVVCISALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLDQSTLESEDTPDSCRRM 118
DB 100 G-----MFQLHLQ-----KELAELESTSQMHTA----- 124
QY 119 KOAFQAVQKELOHIVGQRFSGAPAMMEISWLDVAQRKGPEAQPPAHLT--INAAISIPS 176
DB 125 -----SSLEKQIGHPSPPPE-----KKELRKVAHLTGKSNRSM- 159
QY 177 GSHKVTLSWYHGRGWAKISNNMTLSNGLKLVNQDGFYILYANICFRHHTSGSVPTDYLQ 236
DB 160 -----LEWEDTYGIVLLSGVYKKGGLVINETGLFYVYKVFYRQSCNN-----LP 206
QY 237 LMVYVVKTSIKIPSSHNLMKGGSTKNWGSIEPHFYINVGFFFKLRAGEEISIOVSNPS 296
DB 207 LSHKVMNRNSKYPQDLVME-KGMMSYCTTGQWARSYSLGAVFNLTSAHLYVNVSELS 265
QY 297 LLDPDQDATYFGAFKV 312
DB 266 LVNFEESTFFGLYKL 281
RESULT 11
US-08-815-190A-2
; Sequence 2, Application US/08815190A

Patent No. 6046310
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Schneider, William P.
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,190A
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/614,584
; FILING DATE: 13-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 011823-006710US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-815-190A-2
Query Match 10.4%; Score 173.5; DB 3; Length 281;
Best Local Similarity 21.2%; Pred. No. 2.4e-09;
Matches 67; Conservative 42; Mismatches 108; Indels 99; Gaps 9;
QY 22 PGVPHGGLHPAPSAPAPPPAASR-----SMFLALLGLGL 58
DB 40 PGQRRPPPPPPPPPPPPPPPLPLPLPLKKGHNHSTGCLLVMMFFVVLVALVGLGL 99
QY 59 GQVVCISALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLDQSTLESEDTPDSCRRM 118
DB 100 G-----MFQLHLQ-----KELAELESTSQMHTA----- 124
QY 119 KOAFQAVQKELOHIVGQRFSGAPAMMEISWLDVAQRKGPEAQPPAHLT--INAAISIPS 176
DB 125 -----SSLEKQIGHPSPPPE-----KKELRKVAHLTGKSNRSM- 159
QY 177 GSHKVTLSWYHGRGWAKISNNMTLSNGLKLVNQDGFYILYANICFRHHTSGSVPTDYLQ 236
DB 160 -----LEWEDTYGIVLLSGVYKKGGLVINETGLFYVYKVFYRQSCNN-----LP 206
QY 237 LMVYVVKTSIKIPSSHNLMKGGSTKNWGSIEPHFYINVGFFFKLRAGEEISIOVSNPS 296
DB 207 LSHKVMNRNSKYPQDLVME-KGMMSYCTTGQWARSYSLGAVFNLTSAHLYVNVSELS 265
QY 297 LLDPDQDATYFGAFKV 312
DB 266 LVNFEESTFFGLYKL 281
RESULT 12

APPLICANT: RENSCHAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
TITLE OF INVENTION: IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,122
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-422-8

Query Match 10.2%; Score 171.5; DB 1; Length 261;
Best Local Similarity 25.2%; Pred. No. 3.4e-09;
Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;
QY 33 APSAPAPAPPPAASRSMFLALLGLGQVVCISIALF-LYFRAQMDPNRISEDSTHCFYRI 91
Db 9 SPRSAATGLP--ISMKIFMYLLTVFLITMIGSALFAVYLHRRLD--KIEDER----- 57
QY 92 LRLHE-----NAGLDSTLESEITLPDSCRMRKQAFQAVQKELQHLVGPQRF 140
Db 58 -NLHEDFVFMKTIQRCNTGERSLSLL-----NCEIKSQEGFV-KDIM-----LN 101
QY 141 GAPAMEGSWLDVAQRKPEAQPFALHT:NAASIPSGSHKVTLSWYHDRGWAKISN--M 198
Db 102 KEETKENSEF--EMQKGDQNPQIAAHV-----ISEASKTTSVLQWAEKGYTMSNNLV 153
QY 199 TLSNGK-LRVNODGFYLYANICF-RHHITSGSVPTDYQLQMLVYVVKTSIKIPSSH--L 254
Db 154 TLENGKQLTVKRGQGLYIYAQVTFCSNRRIASSQAP-----FIASLCLKSPGRFERIL 205
QY 255 MKGGSTKNWGSNHFHYINVGFFKLAGREISIQVSNPSSLDDPDQDATYFGAFKV 312
Db 206 LRAANTH--SSAKPCGQSIHLGGVFEL(PGASVFVNVDTPSOVSHGTGFTSGLLKL 261

RESULT 15
US-08-360-923A-2
Sequence 2, Application US/08360923A
Patent No. 5674492
GENERAL INFORMATION:
APPLICANT: FANSLAW, WILLIAM

APPLICANT: LONGO, DAN L.
APPLICANT: MURPHY, WILLIAM
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Apple Macintosh System 7.1
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,923A
FILING DATE: December 21, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-360-923A-2

Query Match 10.2%; Score 171.5; DB 1; Length 261;
Best Local Similarity 25.2%; Pred. No. 3.4e-09;
Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;
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Db 102 KEETKENSEF--EMQKGDQNPQIAAHV-----ISEASKTTSVLQWAEKGYTMSNNLV 153
QY 199 TLSNGK-LRVNODGFYLYANICF-RHHETSGSVPTDYQLQMLVYVVKTSIKIPSSH--L 254
Db 154 TLENGKQLTVKRGQGLYIYAQVTFCSNRRIASSQAP-----FIASLCLKSPGRFERIL 205
QY 255 MKGGSTKNWGSNHFHYINVGFFKLAGREISIQVSNPSSLDDPDQDATYFGAFKV 312
Db 206 LRAANTH--SSAKPCGQSIHLGGVFEL(PGASVFVNVDTPSOVSHGTGFTSGLLKL 261

Search completed: December 29, 2000, 03:57:31
Job time: 32935 sec

OM of: US-08-989-362-2 to: GenEmbl.* out_format : pfs

Date: Dec 29, 2000 12:16 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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Search information block:

Query: US-08-989-362-2

Query length: 316

Database: GenEmbl.*

Database sequences: 1033670

Database length: ~211117393

Search time (sec): 1030.330000

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gb_ro:AB036798	+	1675.00	2428.84	3.6e-127	951 ! AB036798 Mus musculus mRNA for
gb_ro:AF013170	+	1675.00	2421.78	9.0e-127	2237 ! AF013170 Mus musculus TNF-rela
gb_pat:AF062119	+	1675.00	2421.57	9.3e-127	2295 ! AF062119 Sequence 6 from patent
gb_ro:AF053713	+	1675.00	2421.55	9.3e-127	2299 ! AF053713 Mus musculus osteop
gb_ro:AF019048	+	1668.00	2411.64	3.3e-126	2225 ! AF019048 Mus musculus receptor
gb_ro:AB032771	+	1476.50	2140.98	3.9e-111	864 ! AB032771 Mus musculus RANKL 2 m
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gb_pr3:AF013171	+	1101.00	1588.79	2.3e-80	1823 ! AF013171 Homo sapiens TNF-rela
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gb_ro:AB022036S2	+	286.00	414.89	5.5e-15	468 ! AB022037 Mus musculus DNA for c
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gb_pr6:HSU37518	+	260.50	366.83	2.6e-12	1769 ! U37518 Human TNF-related apopt
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gb_hlg3:AC010969	+	215.50	262.62	1.7e-06	194030 ! AC010969 Homo sapiens chrom
gb_pat:BTCD40LIG	+	185.50	263.69	1.5e-06	864 ! 248469 B.taurus mRNA for CD40 l
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gb_ro:RN003470	+	183.00	254.85	4.5e-06	1623 ! U03470 Rattus norvegicus Fas a
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em_pat:E11355	+	182.00	258.02	3.0e-06	927 ! E11355 Mouse cDNA encoding Fas
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em_pat:E11354 + 173.50 245.68 1.5e-05 924 ! E11354 Human cDNA encoding F
gb_pr6:HSU11821 + 173.50 245.26 1.5e-05 972 ! U11821 Human Fas ligand (Fas
gb_pat:AB7645 + 173.50 240.22 2.9e-05 1790 ! AB7645 Sequence 3 from Pat

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seq_documentation_block:
LOCUS AB008426 951 bp mRNA ROD 02-MAY-1998
DEFINITION Mus musculus mRNA for osteoclast differentiation factor (ODF),
complete cds.
ACCESSION AB008426
VERSION AB008426.1 GI:3041781
KEYWORDS osteoclast differentiation factor (ODF).
SOURCE Mus musculus bone marrow stromal cells cell_line:ST2 cDNA to mRNA,
clone_lib:pcDL-SRA296 clone:pOBM291.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 951)

AUTHORS Yasuda,H.

TITLE Direct Submission

JOURNAL

Submitted (22-OCT-1997) to the DDBJ/EMBL/GenBank databases.
Hisataka Yasuda, Snow Brand Milk Products Co., Ltd., Research
Institute of Life Science, 519 Shimo-Ishibashi, Ishibashi-machi,
Tochigi 329-05, Japan (E-mail:fvbd7042emb.infoweb.or.jp,
Tel:0285-52-1331, Fax:0285-53-1314)

REFERENCE 2 (sites)

AUTHORS Yasuda,H., Shima,N., Nakagawa,N., Yamauchi,K., Kinoshita,M.,

Mochizuki,S., Tomoyasu,A., Yano,K., Goto,M., Murakami,A., Tsuda,E.,
Morinaga,T., Higashio,K., Udagawa,N., Takahashi,N. and Suda,T.
Osteoclast differentiation factor is a ligand for
osteoprotegerin/osteoclastogenesis-inhibitory factor and is
identical to TRANCE/RANKL
Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998)

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misc_feature 454..948

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BASE COUNT 231 a 267 c 248 g 205 t

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Ratio: 5.301 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

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US-08-989-362-2 x AB008426 ..

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LOCUS AB036798 951 bp mRNA ROD 29-JUN-2000
DEFINITION Mus musculus mRNA for RANKL 1, complete cds.
ACCESSION AB036798
VERSION AB036798.1 GI:8843829

KEYWORDS RANKL 1.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 951)
AUTHORS Ikeda,T.

TITLE RANKL 1

JOURNAL Published Only in DataBase (2000) In press
REFERENCE 2 (bases 1 to 951)
AUTHORS Ikeda,T.

TITLE Direct Submission

JOURNAL Submitted (11-JAN-2000) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)

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Ratio: 5.301 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

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Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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seq documentation_block: 2295 bp DNA PAT 29-SEP-1999
LOCUS AR062119
DEFINITION Sequence 6 from patent US 5843678.
ACCESSION AR062119
VERSION AR062119.1 GI:5989810
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2295)
AUTHORS Boyle,W.J.
TITLE Osteoprotegerin binding proteins
JOURNAL Patent: US 5843678-A 6 01-DEC-1998;
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51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe 67
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AUTHORS Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R.,
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Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparello,C., Eli,A.,
Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J.,
Delaney,J. and Boyle,W.J.
TITLE Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
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AUTHORS Boyle,W.J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
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 Anderson, D.M., Maraskovsky, E., Billingsley, W.L., Dougall, W.C.,
 Tonetsko, M.E., Roux, E.R., Teepe, M.C., DuBoise, R.F., Cosman, D. and
 Galibert, L.
 A homologue of the TNF receptor and its ligand enhance T-cell
 growth and dendritic-cell function
 Nature 390 (6656), 175-179 (1997)
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 2 (bases 1 to 2225)
 Anderson, D.M., Billingsley, W., Dougall, W., Maraskovsky, E.,
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 Direct Submission
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 Ikeda, T.
 TITLE Receptor activator of NF-kB ligand 2
 JOURNAL Published Only in DataBase (2000) In press
 REFERENCE 2 (bases 1 to 864)
 Ikeda, T.
 TITLE Direct Submission
 JOURNAL Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)

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            Galibert,L.
            A homologue of the TNF receptor and its ligand enhance T-cell
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            Nature 390 (6556), 175-179 (1997)
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149	SerTrpLeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAl	165
576	TCATGGTTAGATCTGGCCAAAGAGGAGCAAGCTTGAAGCTCAGCGT	625
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626	TCATCTCATATAATTAATGCGCACCGACATCCCATCTGGTTCCCAT	675
182	hrLeuSerSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMet	198
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ACCESSION AF053712
VERSION AF053712.1 GI:3057145
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2271)
AUTHORS Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
Delaney, J., and Boyle, W.J.
TITLE Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2271)
AUTHORS Boyle, W.J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
FEATURES
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34 roSerAlaProAlaProAlaProProAlaAlaSerArgSerMetPhe 50
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782 ACTTTTAGCAATGGAAACATAATAGTAAATCAGAGATGGCTTTTATTACCT 831
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832 GTATGCCAACATTTGCTTCGACATCATGAATCTCAGGAGACCTAGCTA 881
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LOCUS AB032772 754 bp mRNA ROD 29-JUN-2000
DEFINITION Mus musculus RANKL 3 mRNA for receptor activator of NF-kB ligand 3,
complete cds.
ACCESSION AB032772
VERSION AB032772.1 GI:8843824
KEYWORDS receptor activator of NF-kB ligand 3.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Ikeda,T., Takahashi,H. and Hirokawa,K.
Somatostatin, a new marker of osteoblast, regulates the expression
of RANKL isoforms
Unpublished (1999)
2 (bases 1 to 754)
Ikeda,T.
Direct Submission
Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tooru
Ikeda, School of Medicine, Tokyo Medical and Dental University,
Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113-8519, Japan (E-mail:tooru.pth2@med.tmd.ac.jp,
Tel:81-3-5803-5176, Fax:81-3-5803-0123)
Location/Qualifiers

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ORIGIN

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92 uArgLeuHisGluAsnAlaGlyLeuGlnA: pSerThrLeuGluSerGluA 109
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seq_documentation_block:

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DEFINITION Homo sapiens mRNA for SODF/TRANCE, complete cds.
ACCESSION AB037599
VERSION AB037599.1 GI:6863047
KEYWORDS SODF/trance; SODF/TRANCE.
SOURCE Homo sapiens male tongue epithelial-like squamous cell carcinoma
cell_line:SCC-4 CDNA to mRNA.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (sites)

Nagai,M., Kyakumoto,S. and Sato,N.

Cancer cells responsible for humoral hypercalcemia express mRNA

encoding a secreted form of ODF/TRANCE that induces osteoclast

formation

Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)

JOURNAL

MEDLINE

20175237

2 (bases 1 to 930)

Nagai,M., Kyakumoto,S. and Sato,N.

Direct Submission

Submitted (26-JAN-2000) to the DDBJ/EMBL/GenBank databases.

Masazumi Nagai, Iwate Medical University School of Dentistry,

Department of Biochemistry; 19-1 Uchinamaru, Morioka, Iwate 020-8505,

Japan (E-mail:mnagai@iwate-med.ac.jp, Tel:+81-19-651-5111(ex.4436),

Fax:+81-19-654-4147)

Location/Qualifiers

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DEFINITION Homo sapiens TNP-related ligand TRANCE mRNA, partial cds.
ACCESSION AF013171
VERSION AF013171.1 GI:2411499
KEYWORDS

SOURCE

ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1823)

AUTHORS
Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlinick,J., Chao,M.,
Kalachikov,S., Cayani,E., Bartlett,F.S. III, Frankel,W.N., Lee,S.Y.
and Choi,Y.

TITLE
TRANCE is a novel ligand of the tumor necrosis factor receptor

JOURNAL
family that activates c-Jun N-terminal kinase in T cells

MEDLINE
J. Biol. Chem. 272 (40), 25190-25194 (1997)

REFERENCE 2 (bases 1 to 1823)

AUTHORS
Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.

Direct Submission

TITLE
Submitted (09-JUL-1997) Howard Hughes Medical Institute, The

JOURNAL
Rockefeller University, 1230 York Ave., New York, NY 10021, USA

FEATURES

Location/Qualifiers

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ORIGIN

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|||||.....:|||||.....:|||||.....:|||||.....:|||||.....
12485 TAAACACAGATCAAAATCCCAAGTTCTCT:ATACCTGATCAAGAGGAGAA 12436

259 erThrLysAsnTrpSerGlyAsnSerGluIuPheHisPheTyrSerIleAsn 275
|||||.....:|||||.....:|||||.....:|||||.....:|||||.....
12435 GCACCAAGTATTGCTCAGGGAATTCGAA::TCCATTTTATTCCATAAAC 12386

276 ValGlyGlyPhePheLysLeuArgAlaGly:GluGluIleSerIleGlnVa 292
|||||.....:|||||.....:|||||.....:|||||.....:|||||.....
12385 GTTGGTGGAATTTTAAAGTTACCGTCTGGTGAGGAATACAGTCGAGGT 12336

292 lSerAsnProSerLeuLeuAspProAspGlnAspAlaThrTyrPheGlyA 309
|||||.....:|||||.....:|||||.....:|||||.....:|||||.....
12335 CTCCAACCCCTCTACTGATCGGATCTGGATGCAACATACTTTGGGG 12286

309 laPheLysValGlnAspIleAsp 316
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12285 CTTTAAAGTTCGAGATATAGAT 12263

seq_name: gb_hgt18:AL139382

seq_documentation_block:

LOCUS AL139382 205139 bp DNP, HTG 06-JUL-2000
DEFINITION Homo sapiens chromosome 13 clone RP11-86N24, *** SEQUENCING IN
PROGRESS ***, 27 unordered pieces.

ACCESSION AL139382

VERSION AL139382.4 GI:8978069

KEYWORDS HTG: HTGS_PHASE1.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 205139)

REFERENCE

AUTHORS Burton,J.

TITLE Direct Submission

JOURNAL Submitted (05-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On Jul 7, 2000 this sequence version replaced gi:8388479.

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: ba86N24

----- Summary Statistics

Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 185877 bases at least Q40
Consensus quality: 193731 bases at least Q30
Consensus quality: 198268 bases at least Q20
Insert size: 202539; sum-of-contigs
Insert size: 162413; 9.2% error; agarose-fp
Quality coverage: 3.08x in Q20 bases; sum-of-contigs Quality
coverage: 3.84x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 19230: contig of 19230 bp in length
* 19231 19330: gap of 100 bp
* 19331 32371: contig of 13041 bp in length
* 32372 32471: gap of 100 bp
* 32472 34870: contig of 2399 bp in length
* 34871 34970: gap of 100 bp
* 34971 42014: contig of 7044 bp in length
* 42015 42114: gap of 100 bp
* 42115 50153: contig of 8039 bp in length
* 50154 50253: gap of 100 bp
* 50254 56692: contig of 6439 bp in length
* 56693 56792: gap of 100 bp
* 56793 61250: contig of 4458 bp in length
* 61251 61350: gap of 100 bp
* 61351 62561: contig of 1211 bp in length
* 62562 62661: gap of 100 bp
* 62662 75173: contig of 12512 bp in length
* 75174 75273: gap of 100 bp
* 75274 81438: contig of 6165 bp in length
* 81439 81538: gap of 100 bp
* 81539 87285: contig of 5747 bp in length
* 87286 87385: gap of 100 bp
* 87386 89590: contig of 2205 bp in length
* 89591 89690: gap of 100 bp
* 89691 91525: contig of 1835 bp in length
* 91526 91625: gap of 100 bp
* 91626 106940: contig of 15315 bp in length
* 106941 107040: gap of 100 bp
* 107041 115418: contig of 8378 bp in length
* 115419 115518: gap of 100 bp
* 115519 119162: contig of 3644 bp in length
* 119163 119262: gap of 100 bp
* 119263 121311: contig of 2049 bp in length
* 121312 121411: gap of 100 bp
* 121412 129170: contig of 7759 bp in length
* 129171 129270: gap of 100 bp
* 129271 141607: contig of 12337 bp in length
* 141608 141707: gap of 100 bp
* 141708 152435: contig of 10728 bp in length
* 152436 152535: gap of 100 bp
* 152536 158440: contig of 5905 bp in length
* 158441 158540: gap of 100 bp
* 158541 159553: contig of 1013 bp in length
* 159554 159653: gap of 100 bp
* 159654 164333: contig of 4680 bp in length
* 164334 164433: gap of 100 bp
* 164434 182240: contig of 17807 bp in length
* 182241 182340: gap of 100 bp
* 182341 183761: contig of 1421 bp in length
* 183762 183861: gap of 100 bp
* 183862 188214: contig of 4353 bp in length
* 188215 188314: gap of 100 bp

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* 188315 205139: contig of 16825 bp in length.
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US-08-989-362-2 x ALL139382 ..
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135090 ACAGGTTCCCAATAAGTGAGTCGTCTCTTGGTACCATGATCGGGTTG 135139
192 pLaLysIleSerAsnMetThrLeuSerAsnGlyLysLeuArgValAsnG 209
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135140 GGCCAAGATCTCCACATGACTTTTAGCAATGGAATACTAATAGTTAATC 135189
209 lnaSpGlyPheTyrTyrLeuTyrAlaAsnIleCysPheArgHisHisGlu 225
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135190 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAA 135239
226 ThrSerGlySerValProThrAspTyrLeuGlnLeuMetValTyrValVa 242
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135240 ACTTCAGGAGACCTAGCTACAGAGATATCTTCAACTAATGGTGACGTAC 135289
242 llyThrSerIleLysIleProSerSerHisAsnLeuMetLysGlyGlyS 259
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135290 TAAACACGATCAAAATCCAAAGTTCTCATACCTGATGAAGAGGAGAA 135339
259 erThrLysAsnTrpSerGlyAsnSerGluPheHisPheTyrSerIleasn 275
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
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276 ValGlyGlyPhePheLysLeuArgAlaGlyGluGluIleSerIleGlnVa 292
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135390 GTTGGTGGATTTTTTAAGTTACCGTCTGGAGAGAAATCAGCATCGAGGT 135439
292 lSerAsnProSerLeuLeuAspProAspGlnAspAlaThrTyrPheGlyA 309
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135440 CTCCACACCCCTCCTTACTGGATCCGGATCAGGATCGAACAATACTTTGGGG 135489
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seq_documentation_block:

seq_documentation_block.
ID V69900 standard; cDNA to mRNA: 951 BP.

CONFIDENTIAL.
CS
XX
XX

FN W05840044+AL.
YY

PD 22-00T-1998.

PF 15-APR-1998; 98WO-JP01728.

PR 02-DEC-1997; 97JP-0332241.

PR 12-AUG-1997; 97JP-0217897;

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PR 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
XX Goto M, Higashio K, Kinosaki M, Kobayashi F, Morinaga T;
PI Nakaqawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E,
PI Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
XX WPI: 1998-594563/50.
DR
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
PT for, e.g. treatment and investigation of disorders of bone and
PT calcium metabolism
PT
XX
XX Disclosure; Pages 116-117; 151pp; Japanese.
XX
XX The present sequence appears in the specification, which describes
CC an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
CC The protein promotes and supports the separation and maturation of
CC osteoclasts in the presence of bone absorption factors such as
CC calcitriol or parathyroid hormone (PTH). OBM is isolated from
CC stroma cells cultured in the presence of a bone absorption factor
CC by separation and solubilisation of membrane proteins then affinity
CC chromatography using OCIF. It exists in a full-sequence form and a
CC solubilised form (SOBM) which is a shorter chain. OBM may be used
CC for screening potential inhibitors and modifiers of its biological
CC activity, and screening for receptors to OBM which mediate its function.
CC These substances can then be used in the treatment of disorders of bone
CC function and calcium metabolism. The antibodies can be used for assay
CC of the protein, for investigative and diagnostic purposes, and as
CC components of drugs.
XX
XX Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;
SQ

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  Percent Identity: 100.000
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US-08-989-362-2 x V69900

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17 uMetGlySerGlyProGlyValProHisG: uGlyProLeuHisProAlap 34
|||||
51 GATGGCGAGCGCGCGCGCTCCACACGAGGGTCCGCTGCACCCCGCGC 100
34 roSerAlaProAlaProAlaProProProlaAlaSerArgSerMetPhe 50
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101 CTCTCTCACCGGCTCGCGCGCGCCACCCXCCGCTCCCGCTCCATGTT 150
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlyValValCysSerIleAlaLe 67
|||||
151 CTGGCCCTCTCTGGGCTGGGACTGGGCGACGTGGTCTGCAGCATCGCT 200
67 uPheLeuTyrPheArgAlaGlnMetAspP: oAsnArgIleSerGluAsp 84
|||||
201 GTTCCTGTACTTTCGAGCGCAGATGGATCTACAGATATATCAGAGACA 250
84 erThrHisCysPheTyrArgIleLeuArgIleuHisGluAsnAlaGlyLeu 100
|||||
251 GCACCTCACTGCTTTATAGAACTCCTGAGACTCCATGAAACCGCAGGTT 300
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
|||||
301 CAGGACTCGACTCTGGAGAGTGAAGACACACTACCTGACTTCCTGCAGG 350
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIle 134
|||||
351 GATGAACACAGCTTTTCAGGGGCGCTGCAGAGGAACTGCAACACATTG 400
134 alcGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
|||||
401 TGGGGCCACAGCGCTTCTCAGGAGCTCCAGCTATGATGGAAGCGTCATG 450
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
|||||
451 TTGGATGTGGCCAGGAGGAGCAAGCGCTGAG3CCAGGCCATTTTCACAC 500
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeus 184
|||||
501 CACCATCATGTGCCAGCATCCCATCGGGFTCCCATAAAGTCACCTGT 550
184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
|||||
551 CCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTA 600
201 SerAsnGlyLysLeuArgValAsnGlnAsp: yPheTyrTyrLeuTyrAl 217
|||||
601 AGCAACGGAAACTAAGGGTTTACCAAGAT:GCTTCTATTACCTGTACGC 650
217 aAsnIleCysPheArgHisGlnThrSe: GlySerValProThrAspP 234
|||||
651 CAACATTGCTTTCGGCATCATGAACATC:GGAAGCGTACCTTACAGACT 700
234 yrLeuGlnLeuMetValTyrValValLysTr: rSerIleLysIleProSer 250
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701 ATCTTCAGCTGATGGTGTATGCTGTTAAAA: CAGCATCAAAATCCCAAGT 750
251 SerHisAsnLeuMetLysGlyGlySerThr: yAsnTrpSerGlyAsnSe 267
|||||
751 TCTCATAACCTGATGAAGAGGAGGAGCAG: AAAAAGTGGTGGGCAATTC 800
267 rGluPheHisPheTyr: SerIleAsnValGL: GlyPhePheLysLeuArgA 284
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801 TGAATTCACCTTTTATTCATAAATGTTGG:GGATTTTTCAGGCTCCGAG 850

284 laGlyGluGluIleSerIleGlnValSerAsnProSerIleuLeuAspPro 300
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851 CTGCTGAAGAAATAGCATTCAGGTGTCCAAACCCCTCCCTGCTGATCCG 900
301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
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901 GATCAAGATGCGAGCTACTTTGGGGCTTTCAAGTTCAGGACATAGAC 948
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XX Z99965;
XX
XX 25-JUL-2000 (first entry)
XX DNA encoding a murine osteoprotegerin ligand (OPGL).
DE
XX
XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
FH 1..951
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FT /*tag= a
FT /product= "osteoprotegerin ligand"
XX
XX W0200015807-A1.
XX
XX 23-MAR-2000.
XX
XX 13-SEP-1999; 99WO-DK00481.
XX
XX 15-SEP-1998; 98BK-0001164.
XX 02-OCT-1998; 98US-0102896.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
XX Halkier T, Haanling J;
XX
XX WPI: 2000-271444/23.
XX P-PSDB; Y84418.
XX
XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
to treat, prevent and ameliorate osteoporosis -
XX
XX Disclosure; Page 79-81; 110pp; English.
XX
XX The present sequence encodes a murine osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.
XX
XX Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;

alignment_scores:

Quality: 1675.00 Length: 316
Ratio: 5.301 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000
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Align seg 1/1 to: Z99965 from: 1 to: 951
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1 ATGCGCGGGCCAGCCAGACATACGGCAAGTACCCTGCCGACGTCGGAGGA 50
17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
51 GATGGCAGCGGCCCGCGCTCCACAGAGGTCGCTGCACCCCGCGC 100
34 roSerAlaProAlaProAlaProProProAlaLaSerArgSerMetPhe 50
101 CTTCTGCACCGGCTCCGGCGCGCCACCCCGCGCTCCGCTCCATGTC 150
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe 67
151 CTGCCCCCTCTGGGGCTGGGACTGGGCCAGGTGTCTGCACATCGCTCT 200
67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS 84
201 GTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAGAAATATCAGAACA 250
84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
251 GCACCTACTGCTTTATAGATCTCGAGACTCCATGAAACGCGAGTTTG 300
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
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117 qMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
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134 alGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
401 TGGGGCCACAGCGCTTCTCAGGAGCTCCAGCTATGATGAAGGCTCATGG 450
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnPropheAlaHisLe 167
451 TTGGATGTGGCCCGCCAGCGAGGCAAGCCTCAGGCCCGCCAGCCATTGCA 500
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeuS 184
501 CACCATCAATGCTGCCAGCATCCCATCGGGTCCCATAAAGTCACCTCTGT 550
184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
551 CCTCTGTGTACCATCATCGAGCTGGGCCAAGATCTCTACATGACGTTA 600
201 SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl 217
601 AGCAACGGAAAACTAAGGTTAACCAAGATGCTTCTATTACCTCTACGC 650
217 aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspTr 234
651 CAACATTTGCTTTCGGCATCATGAACATCGGAAGCGTACCTACAGACT 700
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251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
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XX AC
XX AC
DT 31-MAR-2000 (first entry)
XX DE Osteoclast formation promoting factor coding sequence.
XX KW OBM-BP; OBM binding protein; osteoclast formation promoting factor;
XX KW bone metabolic disease; osteoporosis; therapy; ss.
XX OS Mus sp.
XX JPI1332581-A.
XX PN 07-DEC-1999.
XX PD 20-OCT-1998; 98JP-0316973.
XX PF 24-MAR-1998; 98JP-0076232.
XX PR (SNOW) SNOW BRAND MILK PROD CO LTD.
XX PA (SANY) SANKYO CO LTD.
XX DR WPI; 2000-091362/08.
XX PT A new protein, a DNA and its application -
XX PS Example 1; Page 13; 18pp; Japanese.
XX CC This sequence encodes the osteoclast formation promoting factor (OBM).
CC The invention relates to an OBM binding protein (OBM-BP). The protein is
CC useful as a preventive and/or treating agent for bone metabolic diseases
CC such as osteoporosis. Substances which inhibit the binding of OBM to
CC OBM-BP can be used as biochemical reagents.
XX
SQ Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;

alignment_scores:
Quality: 1675.00 Length: 316
Ratio: 5.301 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-08-989-362-2 x Z49024 ..
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1 ATGCGCGGGCCAGCCAGACATACGGCAAGTACCCTGCCGACGTCGGAGGA 50
17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
51 GATGGCAGCGGCCCGCGCTCCACAGAGGTCGCTGCACCCCGCGC 100
34 roSerAlaProAlaProAlaProProProAlaLaSerArgSerMetPhe 50
101 CTTCTGCACCGGCTCCGGCGCGCCACCCCGCGCTCCGCTCCATGTC 150


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51  LeuAlaLeuLeuGlyLeuGlyLeuGlyLeuValValValCysSerIleAlaLe 67
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151 CTGGCCCTCTGGGGTGGGACATGGGCCAAGTGGTCTGGCAGCATCGCTCT 200
|||||
67  uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS 84
|||||
201 GTTCCTGTACTTTCGAGCGCAGATGATCTTAACAGATATATCAGAGACA 250
|||||
84  erThrHisCysPheTyrArgIleLeuArgIleHisGluAsnAlaGlyLeu 100
|||||
251 GCACCTCAGTCTTTATAGATCTCTGAGATCCATGAAACGCGAGTTTG 300
|||||
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
|||||
301 CAGGACTCGACTCTGGAGAGTGAAGACAC/CTACCTGACTCTCTCGAGGAG 350
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117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
|||||
351 GATGAACACAGCCCTTCAGGGGCGCGTGC/GAAGGAACCTGCAACACATTG 400
|||||
134 aGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
|||||
401 TGGGGCCACAGCGCTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGG 450
|||||
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
|||||
451 TTGGATCTGGCCCGCAGCGCAAGCCCTGAGCGCCAGCCATTTGCACACCT 500
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167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeuS 184
|||||
501 CACCATCAATGCTGCCAGCATCCCATCGGGTCCCATATAAAGTCACCTGT 550
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184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
|||||
551 CCTCTTGGTACCAGATCGAGGCTGGGCCAAGATCTCTACATGACGTTA 600
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201 SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl 217
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601 AGCAACGGAAACATAAGGGTTAACCAAGAT/3GCTTCTATTACCTGTACGC 650
|||||
217 aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspT 234
|||||
651 CAACATTTGCTTTCCGCATCATGAACATC/3GGAAGCGTACCTACAGACT 700
|||||
234 yrLeuGlnLeuMetValTyrValLysTrSerIleLysIleProSer 250
|||||
701 ATCTTCAGCTGATGGTGTATGCTGTTAANA/CAGCATCAAAATCCCAAGT 750
|||||
251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
|||||
751 TCTCATAAAGCTGATGAAGAGGAGGAGCAG/AAAACTGGTGGGCAATTC 800
|||||
267 rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA 284
|||||
801 TGAATTCACACTTATATCCATAAATGTTGG/3GGATTTTCAAGCTCCGAG 850
|||||
284 laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
|||||
851 CTGGTGAAGAAATATGATCATTCAGGTGTCC/ACCTCTCCCTGGTGATCCG 900
|||||
301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
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901 GATCAAGATGCGACGTACTTTGGGGCTTTC/AAAGTTCAGGACATAGAC 948
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seq_name: /cgn_2/9cndata/geneseq/genes/qn/NA1998.DAT:V69886

seq_documentation_block:

ID V69886 standard; cDNA to mRNA; 1531 bp.

XX

AC V69886;

XX

DT 10-FEB-1999 (first entry)

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XX Nucleic acid encoding an OCIF-binding molecule (OBM).
DE
XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW osteoclast; bone absorption factor; bone disorder; calcium metabolism,
KW ss.
XX Unidentified.
OS
XX Key Location/Qualifiers
FH 125..1075
FT CDS /*tag= a
XX
PN W09846644-A1.
XX
XX 22-OCT-1998.
XX
XX 15-APR-1998; 98WO-JP01728.
XX
XX 02-DEC-1997; 97JP-0332241.
PR 15-APR-1997; 97JP-0097808.
PR 09-JUN-1997; 97JP-0151434.
PR 12-AUG-1997; 97JP-0217897.
PR 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
XX WPI; 1998-594563/50.
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
for, e.g. treatment and investigation of disorders of bone and
calcium metabolism
XX
XX Claim 9; Pages 108-109; 151pp; Japanese.
XX
XX The present sequence encodes an osteoclastogenesis inhibitory factor
(OCIF)-binding molecule (OBM). The protein promotes and supports the
separation and maturation of osteoclasts in the presence of bone
absorption factors such as calcitriol or parathyroid hormone (PTH).
OBM is isolated from stroma cells cultured in the presence of a bone
absorption factor by separation and solubilisation of membrane proteins
then affinity chromatography using OCIF. It exists in a full-sequence
form and a solubilised form (SOBM) which is a shorter chain. OBM may be
used for screening potential inhibitors and modifiers of its biological
activity, and screening for receptors to OBM which mediate its function.
These substances can then be used in the treatment of disorders of bone
function and calcium metabolism. The antibodies can be used for assay
of the protein, for investigative and diagnostic purposes, and as
components of drugs.
XX
SQ Sequence 1538 BP; 382 A; 381 C; 416 G; 359 T; 0 other;

alignment_scores:
Quality: 1675.00 Length: 316
Ratio: 5.301 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-989-362-2 x V69886
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Align seg 1/1 to: V69886 from: 1 to: 1538

1 MetArgArgAlaSerArgAspTyrGlyLysTyrLeuArgSerSerGluG1 17
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125 ATGCCCGCGCCAGCAGACTCGGCAAGTACCTGCGCAGCTCGGAGGA 174
|||||
17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
|||||

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XX	V41489 standard: cDNA; 2191 BP.
XX	
AC	V41489;
XX	
DT	24-SEP-1998 (first entry)
XX	
DE	Nucleotide sequence of mouse 499E9 gene.
XX	
KW	Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
KW	antagonist; autoimmune disorder; rheumatoid arthritis;
KW	systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
KW	acute inflammatory response; antibody; antigen; cancer; ss.
XX	
OS	Mus sp.
XX	
FH	Key Location/Qualifiers
FT	CDS 125..1072
FT	/*tag= a
FT	/product= "mouse 499E9 protein"
XX	
PN	WO9825958-A2.
XX	
PN	18-JUN-1998.
XX	
PD	
XX	
PF	12-DEC-1997; 97WO-US22766.
XX	
PR	13-DEC-1996; 96US-0032846.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Gorman DM, Mattson JD;
XX	
DR	WPI; 1998-348452/30.
DR	P-PSDB; W59654.
XX	
PT	Mouse cell surface antigen, 499E9 protein - used to treat conditions
PT	associated with abnormal physiology or development
XX	
PS	Claim 4; Pages 8-11; 59pp; English.
XX	
CC	This is the nucleotide sequence encoding the mouse 499E9 protein, us
CC	in the method of the invention to treat conditions associated with
CC	abnormal physiology or development. The 499E9 protein is expressed
CC	highly on polarised Th1 T cells, binding of 499E9 to its receptor ma
CC	result in either immune cell expansion or apoptosis. Antagonists of
CC	499E9 may be used to modulate immune responses in abnormal situation
CC	e.g. autoimmune disorders including rheumatoid arthritis, systemic
CC	lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
CC	acute inflammatory responses in which T-cell expansion, activation o
CC	immunological T-cell memory play an important role. The antibodies
CC	can be used to raise anti-idiotypic antibodies which will be useful
CC	in detecting or diagnosing various immunological conditions related
CC	the expression of antigens of 499E9. The antibodies, and fragments
CC	499E9 can be used in the treatment of conditions associated with
CC	abnormal physiology or development, including abnormal proliferation
CC	(e.g. cancerous conditions) or degenerative conditions.
XX	
XX	Sequence 2191 BP; 605 A; 461 C; 518 G; 607 T; 0 other;

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seq_documentation_block:
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17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
192 GATGGGAGCGGCCCGCCGCTCCACAGAGGTCCGTCGACCCCGCGC 241
34 roSerAlaProAlaProAlaProProProAlaLaSerArgSerMetPhe 50
242 CTCTGACCGCTCCGCGCGCCACCGCGCTCCGCTCCATGTTTC 291
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe 67
292 CTGGCCCTCTGGGGCTGGGACTGGGCGAGGTGCTGTCAGCATCGCTCT 341
67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAsp 84
342 GTTCCCTGCTACTTCGAGCGGAGATGGATCCTAACAGAAATATCAGAGACA 391
84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
392 GCACCTCACTGCTTTTATAGAACTCTGAGACTCCATGAAGACGAGTTTG 441
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
442 CAGGACTCGACTCTGGAGACTGAAGACACACTACCTGACTCCTGCAGGAG 491
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
492 GATGAACAACAGCCCTTTCAGGGGGCGGTGCAGAGGAATCTCAACACATTG 541
134 aGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
542 TGGGGCCACAGCCCTTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGG 591
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
592 TTGGATGTGCCCGCAGCGAGGCAAGCTGAGCGCCAGCCATTTCACACCT 641
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeus 184
642 CACCATCAATGCTGCCAGCATCCCATCGGTTGCCATAAAGTCACTCTGT 691
184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
692 CCTCTGGTACCAAGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTA 741
201 SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl 217
742 AGCAACGGAAAACTAAGGTTTAAACAAGATGGCTTCTATTACCTGTACGC 791
217 aAsnIleCysPheArgHisGluThrSerGlySerValProThrAspT 234
792 CAACATTGCTTTCGGCATCATGAACATCGGAAGCGTACCTACAGACT 841
234 yrLeuGlnLeuMetValTyrValLysThrSerIleLysProSer 250
842 ATCTTCAGCTGATGCTGTATGCTGTTAAAAACAGCATCAAAATCCCAAGT 891
251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
892 TCTCATAACTGATGAAGAGGAGGAGCAGAAACCTGGTCGGGCAATTC 941
267 rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA 284
942 TGAATTCACACTTTTATTCATAATGTTGGGGATTTTCAAGCTCCGAG 991
284 laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
992 CTGGTCAAGAAATTAGCATTCAGGTGTCACCAACCTTCCCTGCTGGATCCG 1041
301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
1042 GATCAAGATCGCAGCTACTTTGGGGCTTTCAAAAGTTTCAGGACATAGAC 1089

seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1998.DAT:V70284

seq_documentation_block:

ID V70284 standard; DNA; 2295 BP.

XX

AC V70284;

XX

DT 11-FEB-1999 (first entry)

XX

Human osteoprotegerin binding protein encoding DNA from the 32D-F3 ins.
XX
Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
hypercalcaemia; osteoclast differentiation and activation receptor;
Paget's disease; ss.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers
CDS 158..1108
/*tag= a
/product= "osteoprotegerin binding protein"

FT

WO9846751-A1.

XX

PD 22-OCT-1998.

XX

PF 15-APR-1998; 98WO-US07584.

XX

PR 30-MAR-1998; 98US-0052521.

PR

PR 16-APR-1997; 97US-0842842.

PR

PR 23-JUN-1997; 97US-0880855.

XX

PA (AMGE-) AMGEN INC.

XX

PI Boyle WJ;

XX

XX WPI; 1998-594578/50.

DR

DR P-PSDB; W83194.

XX

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,

PT

PT e.g. treating bone diseases by modulating osteoclast differentiation

XX

XX and for diagnosis

PS

Claim 1; Fig 1; 47pp; English.

XX

CC The present sequence encodes human osteoprotegerin (OPG) binding protein.
Host cells transfected with vectors containing nucleic acid molecules
encoding OPG binding protein are used to produce recombinant OPG binding
protein. OPG binding protein is used in binding assays to determine
osteoprotegerin (OG) in biological samples; to screen for specific
binding agents (particularly agonists and antagonists, including
intracellular proteins); to raise Ab (useful in immunoassays for
detection of OPG binding protein) and to identify compounds that
modulate binding of OPG binding protein to osteoclast differentiation
and activation receptor (ODAR). The nucleic acid molecule encoding OPG
binding protein can be used to detect OPG binding protein-encoding
sequences, e.g. screening for related sequences, also to produce
transgenic animal models, while complementary sequences are used for
antisense regulation of OPG binding protein expression. Modulators of
OPG binding protein, particularly soluble forms of OPG binding protein
or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
disease, periodontal disease, osteoporosis, loosening of prostheses,
optionally in combination with agents that promote bone growth.

XX

SQ Sequence 2295 BP; 648 A; 487 C; 538 G; 622 T; 0 other;

alignment_scores:

Quality: 1675.00 Length: 316
Ratio: 5.301 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

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US-08-989-362-2 x V70284
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17 uMetGlySerGlyProGlyValProHisGlyGlyProLeuHisProAlap 34
208 GATGGCAGCGCGCGCGCGTCCACACG/GGGTCCGCTGCACCCCGCGC 257
34 roSerAlaProAlaProAlaProProProIaAlaSerArgSerMetPhe 50
258 CTTCGTCCAGCGCTCGCGCGCGCCACCC/CGCCCTCCCGCTCCATGTT 307
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyG1: ValValCysSerIleAlaLe 67
308 CTGGCCCTCTCTGGGCTGGGACTGGGCCA GTGGTCTGCAGCATCGCTCT 357
67 uPheLeuTyrPheArgAlaGlnMetAsp; oAsnArgIleSerGluAsps 84
358 GTTCCTGTACTTTCGAGCGCAGATGGATCC/TACAGAATATCAGAGACA 407
84 exThrHisCysPheTyrArgIleLeuArgIleuHisGluAsnAlaGlyLeu 100
408 GCACCTCACTGCTTTTATAGATCTCTGAG/ TCCATGAACAGCAGGTTG 457
101 GlnAspSerThrLeuGluSerGluAspThr LeuProAspSerCysArgAr 117
458 CAGGACTCGACTCTGGAGAGTGAAGACAC/ CTACCTGACTCTCTGCAGGAG 507
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
508 GATGAACAACGCTTTCAGGGGCGCTGG/ GAAGGAACCTGCAACACATTG 557
134 alGlyProGlnArgPheSerGlyAlaPro/ laMetMetGluGlySerTrp 150
558 TGGGGCCACAGCGCTTCTCAGGAGCTCCA/ CTATGATGGAAGGCTCATGG 607
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
608 TTGGATGTGGCCAGCGAGCGAAGCTGA/ GCCAGCCATTTGCACACCT 657
167 uThrIleAsnAlaAaSerIleProSerGlySerHisLysValThrLeus 184
658 CACCATCAATGTGCCAGCATCCCATCGG/ TTCCCATAAAGTCACTCTGT 707
184 exSerTrpTyrHisAspArgGlyTrpAla/ lylsIleSerAsnMetThrLeu 200
708 CCTCTTGGTACCACGATCGAGGCTGGGCG/ AGATCTCTAACATGAGGTTA 757
201 SerAsnGlyLysLeuArgValAlaAsnGlnAsrGlyPheTyrTyrLeuTyrAl 217
758 AGCAACGGAATACTAAGGTTTAACCAAGATGGCTTCTATTACCTGTACGC 807
217 aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspt 234
808 CAACATTTCTCTTCGCGCATCATGAACAT/ CGGAACGCTACCTACAGACT 857
234 yIleGlnIleuMetValTyrValValLysThrSerIleLysIleProSer 250
858 ATCTTCAGCTGATGGTGTATGCTGTTAA/ AACGAGCATCAAAATCCCAAGT 907
251 SerHisAspLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
908 TCTCATACCTGATGAAGAGGGAGCAGCA/ AAAAACTGGTGGGCAATTC 957
267 rGluPheHisPheTyrSerIleAsnValG1yGlyPhePheLysLeuArgA 284
958 TGAATTCACACTTTTATTCCATAAATG/ TGGGATTTTCAAGCTCCGAG 1007
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284 laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
1008 CTGGTGAAGAAATTAGCATTAGGTGTCCAAACCTTCCTCTGGATCCG 1057
301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
1058 GATCAAGATCGGAGGTACTTTGGGGCTTCAAACTTCAGGACATAGAC 1105

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seq_documentation_block:
ID Z99966 standard; DNA; 2299 Bp.
XX Z99966;
XX AC
XX DT 25-JUL-2000 (first entry)
XX DE
XX DNA encoding a murine osteoprotegerin ligand (OPGL).
XX KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
XX KW tumour necrosis factor receptor; type II transmembrane protein;
XX KW osteoclast differentiation; CSF-1; osteoclast activator;
XX KW immune response; osteoporosis; bone resorption; ss.
XX OS Mus musculus.
XX FH
XX Key Location/Qualifiers
XX CDS 170..1120
XX FT /*tag= a
XX FT /product= "osteoprotegerin ligand"
XX PN WO200015807-A1.
XX PD 23-MAR-2000.
XX PF 13-SEP-1999; 99WO-DK00481.
XX PR 15-SEP-1998; 98DK-0001164.
XX PR 02-OCT-1998; 98US-0102896.
XX XX
XX PA (MEBI-) M & E BIOTECH AS.
XX XX
XX PI Halkier T, Haaning J;
XX XX
XX DR WPI: 2000-271444/23.
XX DR P-PSDB: Y84419.
XX PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
XX PT to treat, prevent and ameliorate osteoporosis -
XX PS Disclosure: Page 82-85; 110pp; English.
XX CC The present sequence encodes a murine osteoprotegerin ligand (OPGL).
XX CC Osteoprotegerin is a secreted member of the tumour necrosis factor
XX CC receptor family, which blocks osteoclastogenesis in a dose dependent
XX CC manner. The OPGL protein is synthesised as a type II transmembrane
XX CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
XX CC is a potent osteoclast differentiation factor when combined with CSF-1.
XX CC It is not capable of inducing osteoclast differentiation in the absence
XX CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
XX CC specification describes a method for the in vivo down-regulation of
XX CC OPGL activity in an animal. The method comprises using at least one OPGL
XX CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
XX CC an immune response in the animal. The method and OPGL polypeptide are
XX CC useful for treating, preventing and ameliorating osteoporosis or other
XX CC diseases or conditions characterised by excessive bone resorption.
XX SQ Sequence 2299 BP; 641 A; 494 C; 541 G; 623 T; 0 other;

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Quality: 1675.00 Length: 316
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Ratio: 5.301 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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US-08-989-362-2 x 299966
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17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
220 GATGGCGAGCGGGCCCGCGCTCCACAGAGGGTCCGTCACCCCGCGC 269
34 roSerAlaProAlaProAlaProProAlaAlaSerArgSerMetPhe 50
270 CTCTGACCGCTCCGCGCGCCGCCCGCGCTCCCGCTCCATGTC 319
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe 67
320 CTGCGCCCTCTGGGGCTGGGACTGGCGAGTGGCTGTCGAGCATCGCTCT 369
67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAsps 84
370 GTTCTGTACTTCGACGCGGAGATGGATCTTAACAGAAATATCAGAAGACA 419
84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
420 GCACCTACTCTTTATAGATCTCTGAGACTCCATGAAACGCGAGTTG 469
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
470 CAGGACTCGACTCTGGAGTGAAGACACACTACCTGACTCCTCGCAGGAG 519
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
520 GATGAAACAAAGCCCTTCAGGGGGCGTGCAGAGGAACGTGCAACACATTG 569
134 aGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
570 TGGGGCCACAGCGCTCTCAGGAGCTCCAGCTATGATGAAGGCTCATGG 619
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
620 TTGGATGTGCCCCCAGCAGGACGCTGAGCCCGCCAGCCATTGTCACACCT 669
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeus 184
670 CACCATCAATGCTGCCAGCATCCCATCGGGTTCCTAATAAGTCACTCTGT 719
184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
720 CCTCTTGGTACCAGATCGAGGCTGGGCCAAGATCTCTAATACATACGTTA 769
201 SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl 217
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217 aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspt 234
820 CAACATTTGCTTTCGGCATCATGAACATCGGGAAGCGTACCTACAGACT 869
234 yrLeuGlnLeuMetValTyrValLysThrSerIleLysIleProSer 250
870 ATCTTACAGCTGATGGTGTATGCTGTTTAAACACGACATCAAAATCCCAAGT 919
251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
920 TCTCATAACTGATGAAGGAGGAGGAGCAGCAAAATCGGTGGGCAATTC 969
267 rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA 284

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1070 GATCAAGATGCGACGCTACTTTGGGGCTTTCAAAGTTTCAGACATAGAC 1117
seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1998.DAT:V41377
seq_documentation_block:
ID V41377 standard; cDNA; 1630 BP.
XX V41377;
XX
DT 08-OCT-1998 (first entry)
XX
DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
XX
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 3..887
FT /*tag= a
FT /product= "murine RANKL (ligand for RANK)"
XX
XX WO9828426-A2.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US23775.
XX
XX 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
XX (IMV) IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
XX
XX WFI; 1998-377657/32.
DR P-PSDB; W69956.
XX
XX New isolated ligand for receptor activator of NF-kappa B - used to
XX develop products for augmenting an immune response for inhibiting an
XX inflammatory response and for protection of cells
XX
XX Claim 25; Pages 55-57; 80pp; English.
XX
XX This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
XX activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
XX member of the tumour necrosis factor (TNF) family. A soluble RANK
XX may be used for inhibiting activation of NF-kB, by contacting a cell
XX expressing membrane-associated RANK with a soluble RANK which binds to
XX RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
XX used to induce maturation of dendritic cells and enhance their
XX allo-stimulatory capacity, thereby augmenting an immune response. The
XX soluble RANK polypeptide composition may also be used for regulating an
XX immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
XX may be useful in ameliorating negative effects of an inflammatory
XX response that result from triggering of RANK, e.g. in treating toxic
XX shock or sepsis, graft-versus-host reactions, or acute inflammatory
XX reactions. They can also be used in adjunct therapy for disease
XX characterised by neoplastic cells that express RANK. RANKL polypeptides
XX can also be used to identify inhibitors of RANK and thus inhibitors of
XX an inflammatory response, and also for protecting RANK-expressing cells

CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening.

SQ Sequence 1630 BP; 436 A; 355 C; 319 G; 460 T; 0 other;

alignment_scores:
Quality: 1554.00 Length: 294
Ratio: 5.304 Gaps: 0
Percent Similarity: 99.660 Percent Identity: 99.660

alignment_block:

US-08-989-362-2 x V41377 ..

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39 oAlaProProAlaAlaSerArgSerMetPheLeuAlaLeuGlyL 56
|||||
53 GGCGCGCCACCGCGCTCCCGCTCCCAIGTTCTTGGCCCTCTGGGC 102
|||||
56 euGlyLeuGlyGlnValValCysSerIlelelelelelelelelele 72
|||||
103 TGGAGCTGGGCCAGGTGGCTGCAGCATCGCTCTTCTTCTGTATTCGA 152
|||||
73 AlaGlnMetAspProAsnArgIleSerGluAspSerThrHisCysPheTy 89
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153 GCGCAGATGGATCCTAACAGAAATATCAGAAACACAGCAGCTCAGCTTTA 202
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89 rArgIleLeuArgLeuHisGluAsnAlaGlyLeuGlnAspSerThrLeuG 106
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203 TAGAATCCTGAGACTCCATGNAACACGAGATTGCGAGGACTCGACTCTGG 252
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106 luSerGluAspThrLeuProAspSerCysArgMetLysGlnAlaPhe 122
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253 AGAGTGAAGACACACTACCTGACTCTCTGCA;GAGGATGAACAAGCCTTT 302
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123 GlnGlyAlaValGlnGlyLeuGlnHisIleValGlyProGlnArgPh 139
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303 CAGGGGGCGGTGAGAAAGAACTGCAACAC.VTGTGGGGCCACAGCGCTT 352
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139 eSerGlyAlaProAlaMetMetGluGlySe:TrpLeuAspValAlaGlnA 156
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353 CTCAGAGCTCCAGCTATGATGGAAGGCTC.VTGGTTGGATGTGGCCAGC 402
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503 TCAGGCTGGGCCAAGATCTCTAACATGAC.TTAAGCAACGGGAAACTAA 552
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206 rgValAsnGlnAspGlyPheTyTrpLeuT,rAlaAsnIleCysPheArg 222
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653 GTATGTCGTTAAACACAGCATCAAAATCCCAAGTTCTCTCAACCTGATGA 702
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seq_documentation_block:

ID V41371 standard; cDNA; 1630 BP.

XX V41371;

XX AC

DT 08-OCT-1998 (first entry)

XX NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KW immune response; inflammatory response; toxic shock; sepsis;

KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FT CDS 3..887

FT /*tag= a

FT /product= "murine RANKL (ligand for RANK)"

XX PN W09828424-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23866.

XX PR 14-OCT-1997; 97US-0064671.

XX PR 23-DEC-1996; 96US-0059978.

XX PR 07-MAR-1997; 97US-0813509.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI; 1998-377655/32.

XX DR P-PSDB; W68292.

XX New isolated receptor activator of necrosis factor-kappa B - useful

PT for, e.g. developing products for regulating an immune or

PT inflammatory response, treating toxic shock or sepsis

XX Example 7; Pages 55-57; 80pp: English.

XX This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. Host cells transformed
CC or transfected with an expression vector comprising the RANK encoding
CC nucleic acid can be used to produce recombinant RANK protein. The soluble
CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
CC used for regulating an immune or inflammatory response. Inhibition of
CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
CC of an inflammatory response that result from triggering of RANK, e.g. in
CC treating toxic shock or sepsis, graft-versus-host reactions, or acute

CC inflammatory reactions. They can also be used in adjunct therapy for
CC disease characterised by neoplastic cells that express RANK. The products
CC can also be used for detection and drug screening.

XX
SQ Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

alignment_scores:
Quality: 1554.00 Length: 294
Ratio: 5.304 Gaps: 0
Percent Similarity: 99.660 Percent Identity: 99.660

alignment_block:
US-08-989-362-2 x V41371 ..

Align seg 1/1 to: V41371 from: 1 to: 1630

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56 euGlyLeuGlyGlnValValCysSerIleAlaLeuPheLeuTyrPheArg 72
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89 rArgIleLeuArgLeuHisGluAsnAlaGlyLeuGlnAspSerThrLeuG 106
|||||
203 TAGAATCTGAGACTCCATGAAACGCGAGATTGCGAGACTCGACTCTGG 252
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106 luSerGluAspThrLeuProAspSerCysArgArgMetLysGlnAlaPhe 122
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353 CTCAGGAGCTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCCACG 402
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403 GAGCAAGCCTGAGGCCAGCCATTGTCACACCTCACCATCAATGCTGCC 452
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453 AGCATCCCATCGGTTCCCATAAAGTCACTCTGCTCTTGTGTACACGA 502
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206 rgValAsnGlnAspGlyPheTyrTyrLeuTyrAlaAsnIleCysPheArg 222
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603 CATCATGAACATCGGAGCGGTACTACAGACTATCTTCAGCTGATGGT 652
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239 ltyrValValLysThrSerIleLysIleProSerSerHisAsnLeuMetL 256
|||||
653 GTATGTCGTTAAACACACCATCAAAATCCCAAGTCTTCATATACTGATGA 702
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256 ysGlyGlySerThrLysAsnTrpSerGlyAsnSerGluPheHisPheTyr 272
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703 AAGAGGGAGGACGAGAAACTGGTCGGGCAATTCTGAATCCACTTTAT 752
|||||
273 SerIleAsnValGlyGlyPhePheLysLeuArgAlaGlyGluGluIleSe 289
|||||
753 TCCATAAATGTTGGGGATTTTCAAGCTCGAGCTGGTGAAGAAATTAG 802
|||||
289 rIleGlnValSerAsnProSerLeuLeuAspProAspGlnAspAlaThrT 306
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803 CATTCAGGTGTCACACCTTCCCTGCTGTGGATCCGGATCAAGATCGCGGT 852
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306 yrPheGlyAlaPheLysValGlnAspIleAsp 316
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853 ACTTTGGGCTTTCAAGTTTCAGGACATAGAC 884
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seq_name: /cgcn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V41378

seq_documentation_block:

ID V41378 standard; cDNA; 954 BP.

XX

AC V41378;

XX

DT 08-OCT-1998 (first entry)

XX

DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.

XX

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KW immune response; inflammatory response; toxic shock; sepsis;

KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.

XX

OS Homo sapiens.

XX

EH Key Location/Qualifiers

FT CDS 1..954

FT /tag= a

FT /product= "human RANKL (ligand for RANK)"

XX

PN WO9828426-A2.

XX

PD 02-JUL-1998.

XX

PF 22-DEC-1997; 97WO-US23775.

XX

PR 14-OCT-1997; 97US-0064671.

PR

23-DEC-1996; 96US-0059978.

PR

07-MAR-1997; 97US-0813509.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Anderson DM, Galibert LJ, Maraskovsky E;

XX

DR WPI; 1998-377657/32.

XX

DR P-PSDB; W69957.

XX

PT New isolated ligand for receptor activator of NF-kappa B - used to

PT develop products for augmenting an immune response for inhibiting an

PT inflammatory response and for protection of cells

XX

PS Claim 25; Pages 59-60; 80pp; English.

XX

CC This cDNA encodes a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic

CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening.
XX
SQ Sequence 954 BP; 255 A; 239 C; 221 G; 233 T; 0 other;

alignment_scores:
Quality: 1417.50 Length: 318
Ratio: 4.709 Gaps: 2
Percent Similarity: 94.654 Percent Identity: 84.277
alignment_block:
US-08-989-362-2 x V41378 ..
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34 roSerAlaProAlaProAlaProAlaProAlaSerArgSerMetPhe 50
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98 CGCGCGCGCGCTGGCGCGCACAGCGCCGCCCTCCGCTCCCATGTC 147
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyValValValCysSerIleAlaLe 67
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148 GTGGCCCTCTGGGCTGGGCTGGGCGCAAGTGTCTGCGCGCTGGCCCT 197
67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAsps 84
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198 GTTCTTCTATTTCAGAGCGCAGATGGATCCTAATAGAAATATCAGAACATG 247
84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
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248 GCACCTCACTGATTTATAGAAATTTTTCAGATCCATGAAATGCGAGATTT 297
101 GlnAspSerThrLeuGluSerGluAspTh.....LeuProAspSerCy 115
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115 sArgArgMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnH 132
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348 TAGGAGAATTAACAGCGCTTCAAGGAGTGTGCAAAAGGAATTACAAC 397
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seq_documentation_block:

ID V41372 standard; cDNA; 954 BP.

XX V41372;

AC V41372;

XX 08-OCT-1998 (first entry)

XX NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

XX Immune response; inflammatory response; toxic shock; sepsis;

XX RANKL; RANK ligand; tumour necrosis factor; TNF; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..954

FT /*tag= a

FT /product= "human RANKL (ligand for RANK)"

XX WO9828424-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23866.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0813509.

XX (IMMV) IMMUNEX CORP.

XX PA Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI; 1998-377655/32.

XX P-PSDB; W68293.

XX New isolated receptor activator of necrosis factor-kappa B - useful

XX for, e.g. developing products for regulating an immune or

XX inflammatory response, treating toxic shock or sepsis

XX Example 7; Pages 59-60; 80pp; English.

XX

This cDNA encodes a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products can also be used for detection and drug screening.

XX
SQ Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

alignment_scores:

Quality: 1417.50 Length: 318
Ratio: 4.709 Gaps: 2
Percent Similarity: 94.654 Percent Identity: 84.277

alignment_block:

US-08-989-362-2 x V41372 ..

Align seg 1/1 to: V41372 from: 1 to: 954

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AC: z99964;
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DT: 25-JUL-2000 (first entry)
XX
DE: DNA encoding a human osteoprotegerin ligand (OPGL).
XX
KW: Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW: tumour necrosis factor receptor; type II transmembrane protein;
KW: osteoclast differentiation; CSF-1; osteoclast activator;
KW: immune response; osteoporosis; bone resorption; ss.
XX
OS: Homo sapiens.
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FH: Key Location/Qualifiers
FT: CDS 185..1138
FT: /*tag=a
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XX WO200015807-A1.
XX
XX PD 23-MAR-2000.
XX
XX PF 13-SEP-1999; 99WO-DK00481.
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XX PR 15-SEP-1998; 98DK-0001164.
XX PR 02-OCT-1998; 98US-0102896.
XX
XX PA (WEBI-) M & E BIOTECH AS.
XX
XX PI Halkier T, Haaning J;
XX

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PR 16-APR-1997; 97US-0842842.
PR 23-JUN-1997; 97US-0880855.
XX (AMGE-) AMGEN INC.
XX Boyle WJ;
XX WPI: 1998-594578/50.
DR P-PSDB; W83195.
XX Nucleic acid encoding osteoprotegrin binding protein - useful for,
PT e.g. treating bone diseases by modulating osteoclast differentiation
PT and for diagnosis
XX Claim 1; Fig 4; 47pp; English.
XX The present sequence encodes human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC osteoprotegrin (OG) in biological samples; to screen for specific
CC binding agents (particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
XX Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;

alignment_scores:
Quality: 1417.50 Length: 318
Ratio: 4.709 Gaps: 2
Percent Similarity: 94.654 Percent Identity: 84.277
alignment_block:
US-08-989-362-2 x V70285 ..
Align seg 1/1 to: V70285 from: 1 to: 2274
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34 roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe 50
282 CGCGCGCGCGCTGGCGCGCACAGCCCGCGCGCTCCCGCTCCATGTC 331
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyValValCysSerIleAlaLe 67
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532 TAGGAGAAATTAACAGGCCCTTTCAAGGAGCTGTGCAAAAGGAATTACAAC 581
132 IsIleValGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGly 148
582 ATATCGTTGGATCAGACGACATCAGAGCAGAGAGAGCGATGGTGGATGGC 631
149 SerTTPLeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAl 165
632 TCATGGTTAGATCTGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTC 681
165 ahisLeuThrIleAsnAlaAlaSerIleProSerGlySerHisLysValT 182
682 TCATCTCACTATTAAATGCCACCGACATCCATCTGGTTCCTCAATAAGTGA 731
182 hrLeuSerSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMet 198
732 GTCCTGCTCTTGGTACCATGATCGGGGTTGGCCCAAGATCTCCACATG 781
199 ThrLeuSerAsnGlnLysLeuArgValAsnGlnAspGlyPheTyrTyrLe 215
782 ACTTTTAGCAATGGAAGAACTAATAGTTAATCAGGATGGCTTTTATTACCT 831
215 uTyrAlaAsnIleCysPheArgHisGluThrSerGlySerValProT 232
832 GATGCCAACATTTGCTTTCGACATCATGAACTTCAGGAGACCTAGCTA 881
232 hrAspTyrLeuGlnLeuMetValTyrValLysThrSerIleLysIle 248
882 CAGAGTATCTTCACTAATGGTGTACGTCTCAATAAACACCATCAAAATC 931
249 ProSerSerHisAsnLeuMetLysGlySerThrLysAsnTrpSerG1 265
932 CCAAGTTCTCATACCTGATGAAGAGGAGCAACCAAGTATTGGTCAGG 981
265 yAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPheLysL 282
982 GAATTCGTGAATTCATTTTATTCATAAACGTTGGTGGATTTTAAAGT 1031
282 euArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeu 298
1032 TACGGTCTGGAGAGGAATACAGATCGAGGTCTCCAAACCCCTCTTACTG 1081
299 AspProAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspI1 315
1082 GATCCGGATCAGGATGCAACATACCTTTGGGGCTTTTAAAGTTCGAGATAT 1131
315 eAsp 316
1132 AGAT 1135
seq_name: /cgn2_2/gcdata/geneseq/geneseq/NA1998.DAT.V69887
seq_documentation_block:
ID V69887 standard; cDNA to mRNA; 954 BP.
XX V69887;
AC V69887;
XX 10-FEB-1999 (first entry)
DT Nucleic acid encoding a human OCIF-binding molecule (OBM).
XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
KW human; ss.
XX Homo sapiens.
OS XX

FH Key Location/Qualifiers
FT 1. 954
FT /*tag= a
XX WO9846644-Al.
XX
XX 22-OCT-1998.
XX
XX 15-APR-1998; 98WO-JP01728.
XX
XX 02-DEC-1997; 97JP-0332241.
XX
XX 15-APR-1997; 97JP-0097808.
XX
XX 09-JUN-1997; 97JP-0151434.
XX
XX 12-AUG-1997; 97JP-0217897.
XX
XX 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW) SNOW BRAND MILK PROD CO L'D.
XX
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
XX Nakagawa N, Shima N, Takahashi I, Tomoyasu A, Tsuda E;
XX Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
XX WPI; 1998-594563/50.
XX
XX P-PSDB; W83018.
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
XX for, e.g. treatment and investigation of disorders of bone and
XX calcium metabolism
XX
XX Claim 38; Page 115; 151pp; Japanese.
XX
XX The present sequence encodes an osteoclastogenesis inhibitory factor
XX (OCIF)-binding molecule (OBM). The protein promotes and supports the
XX separation and maturation of osteoclasts in the presence of bone
XX absorption factors such as calcitriol or parathyroid hormone (PTH).
XX OBM is isolated from stroma cells cultured in the presence of a bone
XX absorption factor by separation and solubilisation of membrane proteins
XX then affinity chromatography using OCIF. It exists in a full-sequence
XX form and a solubilised form (sOBM) which is a shorter chain. OBM may be
XX used for screening potential inhibitors and modifiers of its biological
XX activity, and screening for receptors to OBM which mediate its function.
XX These substances can then be used in the treatment of disorders of bone
XX function and calcium metabolism. The antibodies can be used for assay
XX of the protein, for investigative and diagnostic purposes, and as
XX components of drugs.
XX
XX Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;
XX
XX
XX alignment_scores:
XX Quality: 1409.50 Length: 318
XX Ratio: 4.698 Gaps: 2
XX Percent Similarity: 94.340 Percent Identity: 83.962
XX
XX alignment_block:
XX US-08-989-362-2 x V69887 ..
XX
XX Align seg 1/1 to: V69887 from: 1 to: 954
XX
XX 1 MetArgAlaSerArgAspTyrGlyLysLysLeuArgSerSerGluG1 17
XX |||
XX 1 ATGCGCGCGGCCAGCAGAGACTACCAAGACCTGGCTCGGAGGA 50
XX
XX 17 uMetGlySerGlyProGlyValProHisGlyGlyProLeuHisProAlap 34
XX |||
XX 51 GATGGCGGCGCGCGGAGCCGAGCCGACGAGACGACCCCTGCAC...GCC 97
XX
XX 34 roSerAlaProAlaProAlaProProAlaAlaSerArgSerMetPhe 50
XX |||
XX 98 CGCGCGCGCGCTGGCGCGCACCACCGCCCTG:CGCCTCCCGCTCCATGTT 147
XX
XX 51 LeuAlaLeuGlyLeuGlyLeuGlyGln/alValCysSerIleAlaLe 67
XX ::::

148 GTGCCCTCTCTGGGGCTGGGGCTGGGCCAGGTTGTCTGCAGCGTGCCT 197
67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAsps 84
198 GTTCTTCTATTTCAGAGCGCAGATGATCCTTAATAGAAATATCAGAAGATG 247
84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
248 GCACCTCATGCATTTATAGAATTTTGAGACTCCATGAAATGCAGATTTT 297
101 GlnAspSerThrLeuGluSerGluAspThr.....LeuProAspSerCy 115
298 CAAGACACAACTCTGGAGAGTCAAGATACAAAATAATACCTGATTCATG 347
115 sArgArgMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnH 132
348 TAGCAGAAATTAACAGCGCTTTCAAGGAGCTGTGCAAAAGGAATTAACAAC 397
132 isIleValGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGly 148
398 ATATCGTTGGATCATCAGCACATCAGAGCAGAGAAAGCGATGGTGCATGCC 447
149 SerTrpLeuaspValAlaGlnArgGlyLysProGluAlaGlnPropheAl 165
448 TCATGGTTAGATCTGGCCAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGC 497
165 aHisLeuThrIleAsnAlaAlaSerIleProSerGlySerHisLysValT 182
498 TCATCTCATTATTAAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGA 547
182 hrLeuSerSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMet 198
548 GTCGTCTCTCTGTACCATCATCGGGTGGGCCAAGATCTCCAACATG 597
199 ThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLe 215
598 ACTTTTAGCAATGGAAGAACTAATAGTTAATCAGGATGGCTTTTATACCT 647
215 uTyrAlaAsnIleCysPheArgHisGluThrSerGlySerValProt 232
648 GTATGCCAACATTTGCTTTCACATCATGAACTTCAGAGACCTTAGCTA 697
232 hrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysIle 248
698 CAGAGTATCTTCAACTAATGCTGTAGCTCACTAAACCAGCATCAAAATC 747
249 ProSerSerHisAsnLeuMetLysGlySerThrLysAsnTrpSerG1 265
748 CCAAGTTCTCATACCTGATGAAAGGAGGAGAACCAAGTATTGGTCAGG 797
265 YasnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysL 282
798 GAATTCGAATTCATTTTATCCATAAAGCTTGGTGGATTTTAAAGT 847
282 euArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeu 298
848 TACGGCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACTG 897
299 AspProAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspI1 315
898 GATCCGGATCAGGATGCAACATACCTTTGGGGCTTTTAAAGTTCGAGATAT 947
315 eASP 316
948 AGAT 951

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 28, 2000, 19:33:49 ; Search time 412.16 Seconds
(without alignments)
48.654 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYLRSSEMGs.....LLDPDQDQTYGAFKVDID 316

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185.5	11.1	261	2 S53090	CD40 ligand - bovi
2	183	10.9	278	2 A49266	fas ligand - rat
3	182	10.9	279	2 A53062	Fas ligand - mouse
4	173.5	10.4	281	2 I38707	Fas ligand - human
5	171.5	10.2	261	2 I53476	CD40 ligand - huma
6	157	9.4	260	2 S21738	CD40 ligand - mous
7	149	8.9	234	1 J01344	tumor necrosis fac
8	146.5	8.7	235	1 OWNSN	tumor necrosis fac
9	143.5	8.6	233	1 S22052	tumor necrosis fac
10	141	8.4	234	1 JH0529	tumor necrosis fac
11	140	8.4	233	1 S11688	tumor necrosis fac
12	139.5	8.3	233	1 QWHUN	tumor necrosis fac
13	137.5	8.2	234	1 A25451	tumor necrosis fac
14	135.5	8.1	235	2 I54490	tumor necrosis fac
15	133.5	8.0	233	1 S24642	tumor necrosis fac
16	133	7.9	185	2 S52715	tumor necrosis fac
17	133	7.9	232	1 S12606	tumor necrosis fac
18	129.5	7.7	235	2 JH0029	tumor necrosis fac
19	129.5	7.7	306	2 I49139	lymphotoxin-beta -
20	117	7.0	244	2 A46066	lymphotoxin beta -
21	115.5	6.9	193	2 S06192	tumor necrosis fac
22	103.5	6.2	340	2 S49742	hypothetical prote
23	103	6.1	3848	2 T17414	TipC protein - sli
24	99.5	5.9	558	2 T23649	hypothetical prote
25	99	5.9	440	2 I49681	glyceraldehyde-3-p
26	97	5.8	450	2 S38114	hypothetical prote
27	95.5	5.7	553	2 B55514	dihydrolipoamide S
28	94	5.6	1486	1 B40333	collagen alpha 1(I
29	93.5	5.6	205	1 QWHUX	lymphotoxin alpha

30	92.5	5.5	197	1 JH0309	tumor necrosis fac
31	92	5.5	549	2 JC5926	secreted klotho pr
32	92	5.5	785	2 T23456	hypothetical prote
33	92	5.5	1012	2 JC5925	membrane klotho pr
34	90.5	5.4	658	2 T39500	serine/threonine-s
35	90	5.4	3011	1 S40770	genome polyprotein
36	89	5.3	1694	2 S50065	sialoadhesin - mou
37	88.5	5.3	202	1 B27303	tumor necrosis fac
38	88.5	5.3	477	2 T38409	adenylyl cyclase-a
39	88.5	5.3	1547	2 JQ0096	hypothetical 176K
40	88	5.3	347	2 H75253	hypothetical prote
41	88	5.3	560	1 J01221	probable 60K inner
42	88	5.3	1420	2 T37781	probable cytoskele
43	88	5.3	2774	2 A43359	microtubule-associ
44	87	5.2	275	2 T01088	tryptophan synthas
45	87	5.2	451	2 T36149	hypothetical prote

ALIGNMENTS

RESULT 1	
S53090	
CD40 ligand - bovine	
C:Species: Bos primigenius taurus (cattle)	
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999	
C:Accession: S53090	
R:Mertens, B.E.L.C.; Muriuki, M.	
submitted to the EMBL Data Library, February 1995	
A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.	
A:Reference number: S53090	
A:Accession: S53090	
A>Status: preliminary	
A:Molecule type: mRNA	
A:Residues: 1-261 <MER>	
A:Cross-references: EMBL:248469; NID:g732569; PIDN:CAA88363.1; PID:g732570	
Query Match 11.1%; Score 185.5; DB 2; Length 261;	
Best Local Similarity 25.1%; Pred. No. 3.3e-08;	
Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps 15;	
QY 32 PAPSAPAPPAPPAASRMFLALLGLGLGVVCSIALF-LYFRAQMDPNRISDSTHCFYR 90	
Db 8 PSPRSVAATGPP--VSMKIFMYLLTAVFLITQMGSAFVYLHRRLD--KIEDER----- 57	
QY 91 ILRLHE-----NAGLQDSTLESEDTLPSCRRMKQAFQAVOKELQHVGPORF 139	
Db 58 --NLHEDFVFMKTIQRCNKGGESL--NCEIRSRFEDLVKDIMQN---REV 104	
QY 140 SGAPAMWEGSLDVAQRCKPEAQPFAHLTINAAIPSGSHKVTLSVWYHDSWAKISN-- 197	
Db 105 KKKEKFE-----MHKGDQEPQIAAHV-----ISEASSKTTSLQWAPKGYTSLNNL 152	
QY 198 MTLNSNGF-LRVNQDGYLYANICF-RHHTSGSVPTDYQLMWVYVWKTISIKPSSH-- 253	
Db 153 VTLENGQLAVKRGFYIYITQVTFCSNREPLSQP-----FIASLCLKSPSGSERI 204	
QY 254 LMKGGSTKNNSGNSEFHYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDQATYFGAFV 312	
Db 205 LLRAANTH--SSSKPCGQOSIHLGVFELQSGASVFNVDPSQVSHGTGFTSFGLLKL 261	
RESULT 2	
A49266	
fas ligand - rat	
C:Species: Rattus norvegicus (Norway rat)	
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999	
C:Accession: A49266	
R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.	
Cell 75, 1169-1178, 1993	
A:Title: Molecular cloning and expression of the Fas ligand, a novel member of the tu	
A:Reference number: A49266; MUID:94084792	

Db 258 LKL 260

RESULT 7

J01344

tumor necrosis factor alpha precursor - horse

N:Alternate names: cachectin; TNF alpha

C:Species: Equus caballus (domestic horse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: J01344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor

A:Reference number: J01344; MUID:92084125

A:Accession: J01344

A:Molecule type: DNA

A:Residues: 1-234 <SU>

A:Cross-references: GB:M64087; NID:gl64244; PIDN:AAA30959.1; PID:gl64245

C:Comment: This protein is an important proximal mediator of endotoxemia.

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 79/1; 95/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane

F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F:19-230/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carboxylate (Ser) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 8.9%; Score 149; DB 1; Length 234;

Best Local Similarity 24.1%; Pred. No. 3.2e-05;

Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

QY 133 IVGPORFSCAPAMGSLDVAQRK-----PEAQPFALHTNAASIPSGSHKVTLSWY 187

Db 55 VIGPQREEQLPNAFO-SINPLAQLTRSSRTPSKPVAHVAN-----PQAEGL-----QWL 106

QY 188 HDRGWAKISN-MTLNSGKLRVNQDGFYILYANICFRHHETSGSVPTDYQLQLMVYVVKTSI 246

Db 107 SGRANALLANGKLTNDQLNQLVPLDGLYLIYSQVLEK-----GQCPDTHVLTITISRLAV 162

QY 247 KIPSSHNLMK-----GSTKNMGNSEHFYISINVGFFKLRAGEEISTQVSN 294

Db 163 SYPSKVNLLSAIKSPCHTESPEQAEPKW-----YEPIYLGGVFQLEKGDLSAEINQ 215

QY 295 PSLD-PQDQATYFG 308

Db 216 PNYLDFAESGQVYFG 230

RESULT 8

QWMSN

tumor necrosis factor alpha precursor - mouse

N:Alternate names: cachectin; TNF alpha

C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000

C:Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696

R:Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.

DNA 7, 193-201, 1988

A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor

A:Reference number: A22908; MUID:88224564

A:Accession: A22908

A:Molecule type: DNA

A:Residues: 1-235 <SHI>

R:Shakhov, A.N.; Nedospasov, S.A.

Bloorg. Khim. 13, 701-705, 1987

A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucleotide sequence

A:Reference number: S03791; MUID:87298639

A:Accession: S03791

A:Molecule type: DNA

A:Residues: 1-235 <SHA>

A:Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087

A>Note: article in Russian with English abstract

R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.

Nucleic Acids Res. 15, 9083-9084, 1987

A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necrosis factor) gene

A:Reference number: A93679; MUID:88067722

A:Accession: A27303

A:Molecule type: DNA

A:Residues: 1-235 <SEM>

A:Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832

R:Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.

Proc. Natl. Acad. Sci. U.S.A. 82, 6050-6064, 1985

A:Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor

A:Reference number: A25164; MUID:85298296

A:Accession: A25164

A:Molecule type: mRNA

A:Residues: 1-235 <PEN>

A:Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085

R:Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, E.

Nucleic Acids Res. 13, 4417-4429, 1985

A:Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression

A:Reference number: A23127; MUID:85242112

A:Accession: A23127

A:Molecule type: mRNA

A:Residues: 1-235 <FRA>

A:Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845

R:Cseh, K.; Beutler, B.

J. Biol. Chem. 264, 16256-16260, 1989

A:Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in two different mature proteins

A:Reference number: A34251; MUID:89380231

A:Accession: A34251

A:Molecule type: protein

A:Residues: 70-87 <CSE>

R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.

Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986

A:Title: Identification of a common nucleotide sequence in the 3'-untranslated region of the murine TNF gene

A:Reference number: I59058; MUID:86149365

A:Accession: I59058

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-230, R', 232-235 <RES>

A:Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083

R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.

Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990

A:Title: Characterization of high molecular weight glycosylated forms of murine tumor necrosis factor

A:Reference number: A36696; MUID:91097531

A:Accession: A36696

A:Molecule type: protein

A:Residues: 80-85, X', 87-99 <SHE>

C:Genetics:

A:Introns: 62/3; 81/1; 97/1

A>Note: the first intron occurs in the 5'-untranslated region

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane

F:80-235/Product: tumor necrosis factor #status experimental <MAT>

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carboxylate (Ser) (covalent) #status predicted

F:86/Binding site: carboxylate (Asn) (covalent) #status predicted

F:148-179/Disulfide bonds: #status predicted

Query Match 8.7%; Score 146.5; DB 1; Length 235;

Best Local Similarity 25.6%; Pred. No. 5.3e-05;

Matches 51; Conservative 36; Mismatches 67; Indels 45; Gaps 11;

QY 133 IVGPORF-----SGAP-----AMMEGSLDVAQRKPEAPFAHLTINAASIPSGSHKVTLS- 184

Db 55 VIGPQREEQLPNAFO-SINPLAQLTRSSRTPSKPVAHVAN-----PQAEGL-----QWL 106

QY 185 SWYHRCWAKISN-MTLNSGKLRVNQDGFYILYANICFRHHETSGSVPTDYQLQLMVYVVKTSI 243

Db 106 EWLQRANALLANGMDLKNQLVPLDGLYLIYSQVLEK-----GQCPDIV-LLTHVTS 159

QY 244 -----TSIKIPSHNLMKGGSTKNMSEHFYSINVGFPKLRAGEIS 290
Db 160 RFAISVQEKVNNLSAVSKPCPKTPGEALKPW-----YEPIYLGGVFOLEKGDQLSA 212
QY 291 QVSNPSLLD-PDQDATYFG 308
Db 213 EVNLPRYLDFAESGVYFG 231

RESULT 9
S22052
tumor necrosis factor alpha precursor - baboon
C:Species: Papio sp. (baboon)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: S22052
R:Sanjanwala, M.; Edwards, A.
A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A:Reference number: S22052
A:Accession: S22052
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <SAS>
A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160
C:Genetics: 62/3; 78/1; 94/1
A:Introns:
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match 8.6%; Score 143.5; DB 1; Length 233;
Best Local Similarity 25.6%; Pred. No. 9.3e-05;
Matches 50; Conservative 36; Mismatches 70; Indels 39; Gaps 11;

QY 133 IVGPQR-FSGAPAMMEGSLDVAORCK---PEAQPPAHITINAAISPSGSHKVTLSWY 187
Db 55 VIGPQREPFKPSLI--SPLAQAVRSSRTPSDKPAHVAVN---PQAEQGL---QWL 105

QY 188 HDRGWAKISN-MTLNSGLRVNODGFFLYLANICFRHETSGSVPTDYQL------M 238
Db 106 NRRANALLANGVELRNQNVPPSEGGLYISQVLFK---GQGPCSTHVLTTHTISRIAV 161

QY 239 VYVVK---TSIKIPSHNLMKGGSTKNMSEHFYSINVGFPKLRAGEISIOVSN 294
Db 162 SYOTKVNLLSAIKSPQRETPEGAELKPW-----YEPIYLGGVFOLEKGDRLSABEINL 214

QY 295 PSLLD-PDQDATYFG 308
Db 215 PDYLDFAESGVYFG 229

RESULT 10
JH0529
tumor necrosis factor alpha precursor - sheep
N:Alternate names: cachectin; TNF alpha
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: JH0529; S48118; S13114; S20661
R:Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with
A:Reference number: JH0529; MUID:92112044
A:Accession: JH0529
A:Molecule type: mRNA
A:Residues: 1-234 <GRE>
A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
A:Experimental source: alveolar macrophage
R:Nash, A.D.; Barham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991

A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A:Reference number: S48118; MUID:92155784
A:Accession: S48118
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <NAS>
A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807
R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A:Reference number: S13114; MUID:91067496
A:Accession: S13114
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62,64-234 <YOU>
A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A:Note: comparison with the introns of homologous sequences suggest that this is prob
C:Superfamily: tumor necrosis factor
C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lym
F:1-77/Domain: propeptide #status predicted <PRO>
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F:20/Binding site: myristate (Lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;
Best Local Similarity 25.8%; Pred. No. 0.00015;
Matches 51; Conservative 31; Mismatches 72; Indels 44; Gaps 11;

QY 133 IVGPQR-FSGAPAMMEGSLDVAORCKPEAQPPAHITINAAISPSG---SHKVTLSWYH 188
Db 55 VIGPQREEQSPA-----GPSENRPLVQ-TLRSSQASNNKPAHVAVVANISAPG 101

QY 189 DRGWA-KTSMNLSNG-KLRVQ-----DGFYLYLANICFRHH-----ETSGSVP 231
Db 102 QLWGDSTYANALMANGVELKNQNVVPTDGLYLYSQVLFGRHGCPSTPLFLTHTISRIA 161

QY 232 TDYQLQMVVVKTSIKIPSHNLMKGGSTKNMSEHFYSINVGFPKLRAGEISIQ 291
Db 162 VSY-QTKVNIL-SAIKSPCHRETLEGAELKPW-----YEPIYQGVFOLEKGDRLSAE 212

QY 292 VSNPSLLD-PDQDATYFG 308
Db 213 INLPEYLDFAESGVYFG 230

RESULT 11
S11688
tumor necrosis factor alpha precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
C:Accession: S11688
R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A:Title: Gene sequence of feline tumor necrosis factor alpha.
A:Reference number: S11688; MUID:91016860
A:Accession: S11688
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MCG>
A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777
C:Genetics: 62/3; 78/1; 94/1
A:Introns:
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match 8.4%; Score 140; DB 2; Length 233;

Best Local Similarity 25.1%; Pred. No. 0.00018;
Matches 50; Conservative 35; Mismatches 74; Indels 40; Gaps 10;

Qy 124 GAVOKELQHIVGPQRSGAPAMMEGSLDVAQRGKPEAQPFahlTINAASIPSGSHKVTL 183
Db : : : | | | :
57 GPQRELPH-GLQLINPLPQTLRSS-----SRTPSDKPVAHVAN-----PEAEGQLOR 104
Qy 184 SSWYHDRGWAKISN-MTLNSGKLVRNQDPFYLYANICFRHHETSGSVPTDYQL'------ 237
Db :
105 LS---RRANALLANGVELTDNLKVPDSGLYLIYSQVLF-----TGQGCPSHVLTHAIS 157
Qy 238 ---MYVVVK-----TSKIPSSHMLMGKGSTKNNGSNEFHFYSINVGGFFKLRAAGEEISI 290
Db :
158 RFAVSQTKVNLLLSATKPCQRETPEGAEAKPW-----YEPIYLGGVFQLEKGRDLSLT 210
Qy 291 QVSNPSSLID-PDODATYFG 308
Db :
211 EINLPAYLDFAESGGQVYFG 229

RESULT 12
QMUN

tumor necrosis factor alpha precursor - human
N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 04-Feb-2000
C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
Nucleic Acids Res. 13, 6361-6373, 1985
A>Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
A:Reference number: A93585; MUID:86016093
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <NED>
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
R:Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A>Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A:Reference number: S36153; MUID:93272029
A:Accession: S36153
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <IR>
A:Cross-references: EMBL:D15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A>Title: Human tumour necrosis factor: precursor structure, expression and homology to l
A:Reference number: A93351; MUID:85086244
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PEN>
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A>Note: This protein was isolated from the monocyte-like cell line HL-60 from a promyeloid
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
Science 228, 149-154, 1985
A>Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A:Reference number: A44189; MUID:85142190
A:Accession: A44189
A:Molecule type: mRNA
A:Residues: 1-62, 'S', 64-233 <WAN>
A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R:Fukuda, S.; Ando, S.; Sanou, O.; Taniat, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
A>Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A:Reference number: A61478; MUID:88301617
A:Accession: B61478
A:Molecule type: protein
A:Residues: 83-102, 109-119; 121-128, 'X', 130-131, 142-144, 'X', 146, 'XX', 150-152; 159-174; 180
R:Marmerout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A>Title: Molecular cloning and expression of human tumor necrosis factor and compariso
A:Reference number: I53311; MUID:86030296

A:Accession: 153311
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <MAR>
A:Cross-references: GB:M26331; NID:g339763; PID:AAA36758.1; PID:g339764
A:Experimental source: U-937 cells
R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A:Title: O-glycosylated species of natural human tumor-necrosis factor-alpha.
A:Reference number: S62610; MUID:96202967
A:Accession: S62610
A:Molecule type: protein
A:Residues: 77-99 <TAK>
R:D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter re
A:Reference number: 154522; MUID:94102809
A:Accession: 154522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <DAL>
R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific
A:Reference number: A59163; MUID:93018820
A:Contents: annotation: identification of myristylated lysines
R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br
J. Biol. Chem. 260, 2345-2354, 1985
A:Title: Human tumor necrosis factor. Production, purification, and characterization.
A:Reference number: A92511; MUID:85130974
A:Contents: annotation: disulfide bond
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc
out detriment to normal cells. It can also act synergistically with interferon gamma
C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clon
ut are produced by different cell types and have different induction kinetics.
C:Genetics:
A:Gene: GDB:TNF; TNFA
A:Cross-references: GDB:120441; OMIM:191160
A:Map position: 6p21.3-6p21.3
A:Introns: 62/3; 78/1; 94/1
C:Complex: homotrimer
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxic; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; m
F:1-76/Domain: propeptide #status predicted <PRO>
F:77-233/Product: tumor necrosis factor #status experimental <MAT>
F:19,20/Binding site: myristate (lys) (covalent) #status experimental
F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F:145-177/Disulfide bonds: #status experimental

Query Match	8.3%;	Score 139.5;	DB 1;	Length 233;
Best Local Similarity	24.9%;	Pred. NO. 0.0002;		
Matches	48;	Conservative 34;	Mismatches 76;	Indels 35; Gaps 9;
Qy	133	IVGPORFSGAPAMBEGSWLDVAQRCK	---	PEAQPF AHLTINAASTIPSGSHKVTLSWYHD 189
		:::	:	:::
Db	55	VIGPQREEFDRDLISLPLAQRSSSTPDKPAHVAVN	----	PQAEQGL--OQLNR 107
Qy	190	RGWAKISN-MTLSNGKLRVNDGFFYLXANICFRHHETSGSVPTDYLQL	-----	WVY 240
		::: ::	:	::: ::
Db	108	RANALLANGVELRDNLQVPSEGLYLIYSVLFK	----	GQGPCSTHVLTTHTISRIASVY 163
Qy	241	VVK-----TSIKIPSSHNLKMGSTKNWGSNSEFHPYYSINVGFFFKLRAGEELISIOVSNPS		296
		::: ::	:	::: ::
Db	164	QTKVNLLSAIIKSPCQRETPEGAERKPW	-----	YEPILGGVFOLEKGRDLSAEINRPD 216
Qy	297	LLD-PDQDATYFG	308	
		::: ::		
Db	217	YLDFAESGVYFG	229	
		::: ::		
RESULT	13			

A25451

tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: A25454; A25451; JS0727
R:Itto, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.
DNA 5, 149-156, 1986
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit tumor necrosis factor
A:Reference number: A25454; MUID:86219711
A:Accession: A25454
A:Molecule type: mRNA
A:Residues: 1-234 <ITO>
A:Cross-references: GB:M12845; NID:gl65759; PIDN:AAA31486.1; PID:gl65760
R:Itto, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A:Reference number: A25451; MUID:86219712
A:Accession: A25451
A:Molecule type: DNA
A:Residues: 1-234 <IT2>
A:Note: This sequence differs from that shown in having a Gln inserted between residues R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
A:Reference number: JH0309; MUID:91065534
A:Accession: JS0727
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62, 'O', 63-234 <SHA>
A:Cross-references: GB:M60340; GB:M35326; NID:gl65754; PIDN:AAA31484.1; PID:gl65756
C:Genetics:
A:Introns: 62/3; 80/1; 96/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane
F:1-81/Domain: propeptide #status predicted <PRO>
F:82-234/Product: tumor necrosis factor #status predicted <MAT>
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:83/Binding site: carboxylate (Ser) (covalent) #status predicted
F:147-178/Disulfide bonds: #status predicted

Query Match 8.2%; Score 137.5; DB 1; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.0003;
Matches 68; Conservative 31; Mismatches 99; Indels 103; Gaps 12;

QY 27 EGPLPAPSAPAPPPAASR-----SMFLALLGLGQVVCSTALFLYFRAQMDPNRIS 81
DB 14 EGPL-----PKKAGPGQSKRCICLSFLVAGATTLC-----LLHFRVIGPQEEES 63
QY 82 EDSTHCFYRILRLHENAGLDQSTLESDTLPSDCRRMKQAFQAVOKELQHVGPQRFSG 141
DB 64 PNNHLV-----NPVAQWVTLRS-----ASRALSDKPLAHV----- 95
QY 142 APAMEGSWLDVAQRKPEAQPFAHLTINAASIPSGSHKVTLSWYHDGWAKISN-MTL 200
DB 96 ANPQVEGQ-----LQWLSQRANALLANGMKL 121
QY 201 SNGKLRVNDGFFLYLANICFRHHETSGSVPTDYQLQMLVYVVTSTKIPSSHNLKMG--- 257
DB 122 TONQLVVPADGLVLYSQVLF-----SGQCRSVLLTHTVSRFVSYPNKVNLLSAIKS 176
QY 258 -----GSTKNWGSNEFFHYSINVGGFFKLRAEETISIOVSNPSLLD-PDQDATYF 307
DB 177 PCHRETPAEAPMAW-----YEPIYLGGVFQLEKGRDRLSTEVNQPEYLDLAESGVYF 229
QY 308 G 308

DB 230 G 230

RESULT 14
154490

tumor necrosis factor alpha precursor - white-footed mouse
C:Species: Peromyscus leucopus (white-footed mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C:Accession: 154490
R:Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus l
A:Reference number: 154490; MUID:92218012
A:Accession: 154490
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C:Genetics:
A:Gene: TNF
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carboxylate (Ser) (covalent) #status predicted

Query Match 8.1%; Score 135.5; DB 2; Length 235;
Best Local Similarity 25.1%; Pred. No. 0.00044;
Matches 51; Conservative 31; Mismatches 68; Indels 53; Gaps 10;

QY 133 IVGPQRFSGAP-----AMMEGSLDVAQRKPEAQPFAHLTINAASIPSGSHKVTLS 185
DB 55 VIGPQREKFPNNLPPIIGSMQTLTLRSSQNSSD-KPVAHVAN-----HQVDEQL 105
QY 186 WYHGRGWAKISNMTLSNG-KLRVNO-----DGFFLYLANICFRHHETSGSVPTDYQLQMV 239
DB 106 EWSLRG-----ANALLANGMDLKNQLVIPADGLVLYSQVLFKGGCQSSV-----LLT 155
QY 240 YVVK-----TSIKPSSHNLKMGSTKNWGSNEFFHYSINVGGFFKLRAE 286
DB 156 HTVSRFAVSYEDKVNLLSAIKSPCKETPEGSELKPW-----YEPIYLGGVFQLEKGD 208
QY 287 EISIQVSNPSLLD-PDQDATYFG 308
DB 209 RLSAEVNLKYLDFAESGVYFG 231

RESULT 15
S24642

tumor necrosis factor alpha precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: 146047; S24642
R:Cludts, I.; Cleuter, Y.; Ketmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
A:Reference number: 146046; MUID:94083525
A:Accession: 146047
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-233 <CL2>
A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
C:Genetics:
A:Gene: TNFA
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carboxylate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match 8.0%; Score 133.5; DB 1; Length 233;
Best Local Similarity 25.8%; Pred. No. 0.00064;
Matches 51; Conservative 30; Mismatches 72; Indels 45; Gaps 11;

QY 133 IVGPQR--FSGAPAMMEGSLDVAQRKPEA---QPFALHTINAASIPSGSHKVTLS 187

```
Db 55 VIGQREESGPGSI--NSPLVQTLRSSQASSNKPVAHVAD-----INSPG 100
Qy 188 HDRGWAKISNMTLSNG-KLRVQ-----DGFYLYLANICFRHH-----ETSGSVP 231
Db 101 QLRWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFRRGQCPSTPLFLTHTISRIA 160
Qy 232 TDYLOLMVYVVKTSIKIPSSHNLMKGGSTKNWGNSEPHFYSINVGGPFKLRAGEEISIQ 291
Db 161 VSY-QTKVNIL-SAIKSPCHRETPEWAEAKPW-----YEPIYOGGVFQLEKGDRLSAE 211
Qy 292 VSNPSLLD-PDODATYFG 308
Db 212 INLPDYLDYAESGOVYFG 229
```

Search completed: December 29, 2000, 08:33:43
Job time: 46794 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 28, 2000, 19:38:36 ; Search time 231.76 Seconds
(without alignments)
43.560 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675
Sequence: 1 MRRASRDYGVKLSSEMGs.....LLDPDQATYCAFKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258.5	15.4	281	1	TRAI_HUMAN
2	244	14.6	291	1	TRAI_MOUSE
3	185.5	11.1	261	1	TNF5_BOVIN
4	183	10.9	278	1	FASL_RAT
5	182	10.9	279	1	FASL_MOUSE
6	173.5	10.4	281	1	FASL_HUMAN
7	171.5	10.2	261	1	TNF5_HUMAN
8	157	9.4	234	1	TNFA_CAVPO
9	157	9.4	260	1	TNF5_MOUSE
10	149	8.9	234	1	TNFA_HORSE
11	148.5	8.9	233	1	TNFA_MACFA
12	147.5	8.8	233	1	TNFA_MACMU
13	146.5	8.7	235	1	TNFA_MOUSE
14	143.5	8.6	233	1	TNFA_PAPHU
15	143.5	8.6	233	1	TNFA_PAPSP
16	141	8.4	234	1	TNFA_SHEEP
17	140	8.4	233	1	TNFA_FELCA
18	139.5	8.3	233	1	TNFA_CANFA
19	139.5	8.3	233	1	TNFA_HUMAN
20	137	8.2	235	1	TNFA_RABIT
21	135.5	8.1	235	1	TNFA_PERLE
22	133.5	8.0	233	1	TNFA_BOVIN
23	133	7.9	232	1	TNFA_PIG
24	129.5	7.7	233	1	TNFA_MARMO
25	129.5	7.7	235	1	TNFA_RAT
26	129.5	7.7	306	1	TNFC_MOUSE
27	128	7.6	229	1	TNFA_CEREL
28	117	7.0	244	1	TNFC_HUMAN
29	115.5	6.9	193	1	TNFA_CAPHI
30	109.5	6.5	233	1	TNFA_MACEU
31	103.5	6.2	340	1	YMD1_YEAST
32	99	5.9	440	1	G3PT_MOUSE
33	97	5.8	450	1	YK22_YEAST

34	95.5	5.7	553	1	ODP2_ALCEU	Q59098	alcaligenes
35	93.5	5.6	205	1	TNFB_HUMAN	P01374	homo sapien
36	92.5	5.5	197	1	TNFB_RABIT	P10154	oryctolagus
37	90.5	5.4	658	1	PAK1_SCHPO	Q62230	mus musculus
38	89	5.3	1694	1	SN_MOUSE	P09225	mus musculus
39	88.5	5.3	202	1	TNFB_MOUSE	P40123	homo sapien
40	88.5	5.3	477	1	CAP2_HUMAN	P50426	capra hircu
41	88.5	5.3	559	1	GLIS_CAPHI	P20951	papaya mosa
42	88.5	5.3	1547	1	RRPO_PMV	P25754	pseudomonas
43	88	5.3	560	1	60IM_PSEPU	P34926	rattus norv
44	88	5.3	2774	1	MAPA_RAT	Q14953	homo sapien
45	85	5.1	304	1	NRK9_HUMAN		

ALIGNMENTS

RESULT 1

ID	TRAI_HUMAN	STANDARD;	PRT;	281 AA.
AC	P50591;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	TNF-RELATED APOPTOSIS INDUCING LIGAND (TRAIL PROTEIN) (APO-2 LIGAND)			
DE	(APO-2L).			
GN	TNFSF10 OR TRAIL OR APO2L.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 96111955.			
RA	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,			
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,			
RA	Goodwin R.G.;			
RT	"Identification and characterization of a new member of the TNF			
RT	family that induces apoptosis.";			
RL	Immunity 3:673-682(1995).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-PLACENTA;			
RA	MEDLINE; 96278649.			
RA	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,			
RA	Ashkenazi A.;			
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor			
RT	necrosis factor cytokine family.";			
RL	J. Biol. Chem. 271:12687-12690(1996).			
CC	-!- FUNCTION: INDUCES APOPTOSIS.			
CC	-!- SUBUNIT: HOMOTRIMER (POTENTIAL).			
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).			
CC	-!- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG			
CC	AND PROSTATE.			
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			

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CC	EMBL; U37518; AAC50332.1; -
DR	EMBL; U57059; AAB01233.1; -
DR	MIN; 603598; -
DR	INTERPRO; IPR000478; -
DR	PFAM; PF00229; TNF; 1.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS50049; TNF_2; 1.
KW	Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT	DOMAIN 1 17
FT	TRANSMEM 18 38
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).
SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;

Query Match 15.4%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred. No. 2.5e-14;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 43 PAASRSMFALLGLGLGQVCSIALFLYFRAQMD--PNRISDSTHCFYRLRHENAGL 100
DB 10 PSLGOTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKGIACE-----LKEDDSY 64
QY 101 QDSTLESDTLDPDCRRMKQAFQAGVOK-----ELQHVGPQRFSGAPAMM 146
DB 65 WDP--NDESNMSPQVQKWLRLVRLMRLTSEETISVQEQKQNISPL----- 113
QY 147 EGSWLDVAQRKPEAQFPAHLT-----NNAASIPSGSHKVTL-----SSWYHDR-GWAKIS 196
DB 114 -----VREPGQVAV--AHITGTRGNTLSPPSKNKKALGRKINSWESSRSGHSPL 165
QY 197 NMTLSNGKLRVNDQGFYLYANICFRHHETSGSVPTDYLQLMVMYVVKTSIKIPSSHNL 256
DB 166 NLHLRNGELVIEHGFYIYSQTYERFOEIKENTKNDQVMQYIYKYT-SYDPDPILLMK 224
QY 257 GGSTKNWGSNBEFHYISNVGGFFKLRAAGEEISIOVSNPSLLDPDODATYFGAFV 312
DB 225 SARNCSWKADEYGLYSIQGGIFELKENDRIFVSVTNEHLMDMDEASFFGAFLV 280

RESULT 2
TRAIL_MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TNF-RELATED APOPTOSIS INDUCING LIGAND (TRAIL PROTEIN).
GN TNFSF10 OR TRAIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9611195.
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.
RT Identification and characterization of a new member of the TNF
family that induces apoptosis.
RL Immunity 3:673-682(1995).
CC -!- FUNCTION: INDUCES APOPTOSIS.
CC -!- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: WIDESPREAD.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; U37522; AAC52345.1; -
DR MGD; MGI:107414; TRAIL.
DR INTERPRO; IPR000478; -
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT DOMAIN 1 17
FT TRANSMEM 18 38
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 14.6%; Score 244; DB 1; Length 291;
Best Local Similarity 27.5%; Pred. No. 4.1e-13;
Matches 83; Conservative 50; Mismatches 111; Indels 58; Gaps 15;

QY 52 ALLGLGLGQ-----VCSIAL-----FLYFRAQMD--PNRISDSTHCFYRIL 92
DB 6 ALKDLFSQHFRMMVICIVLLQVAVVYMYFTNEMKQLQDNYSKIGLACFSK-- 63
QY 93 RLHENAGLQDSTLESDTLDPDC-----RRMKQAFQCAVQKELQHVIG--PQRFSGAPAMM 146
DB 64 ---TDEDFWDS--DGEILNRPCLOVKRQLYQLIEETVLTFTQDTISTVPEKQLSTPLP 118
QY 147 EGSWLDVAQRKPEAQFPAHLT-----NNAASIPSGSHKVTL-----SSWYHDR-GWAKIS 196
DB 119 RG-----GRPO-KVAAHITGTRNSALIPISKDGTLOGKIESWESSRSGHSFLN 169
QY 197 NMTLSNGKLRVNDQGFYLYANICFRHHE---TSGSVPTDYL---QLMVMYVVKTSIKIPS 250
DB 170 HVLFRNGELVIEHGFYIYSQTYERFOEADASKWYKDKVTKQLVOYIYKYT-SYDP 228
QY 251 SHNLKGGSTKNWGSNBEFHYISNVGGFFKLRAAGEEISIOVSNPSLLDPDQDATYFGAF 310
DB 229 PIVLMKSARNCSWSDAEYGLYSIQGGIFELKKNDRIFVSVTNEHLMDLDQEAFFGAF 288
QY 311 KV 312
DB 289 LI 290

RESULT 3
TNFS_BOVIN STANDARD; PRT; 261 AA.
AC P51749;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39).
GN TNFSF5 OR CD40LG OR CD40L.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96006582.
RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;
RT Cloning of two members of the TNF-superfamily in cattle: CD40 ligand and tumor necrosis factor alpha.
RL Immunogenetics 42:430-431(1995).
CC -!- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; Z48469; CAA88363.1; -

RA Suda T., Nagata S.;
 RT "Generalized lymphoproliferative disease in mice, caused by a point
 RL mutation in the Fas ligand.";
 RN Cell 76:969-976(1994).
 [2]
 RP SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELING.
 RC STRAIN=C57BL/6;
 RX MEDLINE: 95388076;
 RA Peitsch M.J., Tschopp J.J.;
 RT "Comparative molecular modelling of the Fas-ligand and other members
 RL of the TNF family.";
 RN Mol. Immunol. 32:761-772(1995).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95196085.
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
 RT Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
 RN "The mouse Fas-ligand gene is mutated in gld mice and is part of a
 RL TNF family gene cluster.";
 RN Immunity 1:131-136(1994).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Fenner M.H., Shioda T., Isselbacher K.J.;
 RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
 RL two amino acids.";
 RN Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 [5]
 RP CHARACTERIZATION OF VARIANT GLD.
 RX MEDLINE: 96091792.
 RA Habne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,
 RT Rousseau M., Bron C., Renno T., French L., Tschopp J.;
 RN "Characterization of the non-functional Fas ligand of gld mice.";
 RL Int. Immunol. 7:1381-1386(1995).
 CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
 CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
 CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
 CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
 CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
 CC T CELLS, OR BOTH.
 CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
 CC -1- SURCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
 CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
 CC SURFACE.
 CC -1- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
 CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
 CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC send an email to license@isb-sib.ch).
 CC
 CC EMBL: U06948; AAA17800.1; -
 CC EMBL: U10984; AAA19778.1; -
 CC EMBL: S76752; AAB33780.1; -
 CC EMBL: U58995; AAB02915.1; -
 CC HSSP: P01375; 2TUN.
 CC MGD: MGI:99255; FASL.
 CC INTERPRO: IPR000478; -
 CC PFAM: PF00229; TNF; 1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;
 CC Disease mutation.
 CC
 CC DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 CC DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 4 69 PRO-RICH.

FT DOMAIN 45 51 POLY-PRO.
 FT DISULFID 200 231 BY SIMILARITY.
 FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 184 184 T -> A (IN STRAIN BALB/C).
 FT VARIANT 218 218 E -> G (IN STRAIN BALB/C).
 FT VARIANT 273 273 F -> L (IN GLD; ABOLISH BIDDING OF FASL TO
 FT ITS RECEPTOR).
 SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;
 Query Match 10.9%; Score 182; DB 1; Length 279;
 Best Local Similarity 22.7%; Pred. No. 5.1e-08;
 Matches 72; Conservative 48; Mismatches 105; Indels 92; Gaps 13;
 QY 13 RSSEEMSGPGVPHGPHAPSAPAPP-----PAASRSMFLALIGLG 57
 DB 38 RGPDRRRPPPPPPVSP-L-PPSQPLPLPLTLPLKKDHTNLWLVVFFMVLVALVGMG 96
 QY 58 LGOVCSIALFLYFRAQMDPNRISDSTHCFYRLRLHFNAGLQDSTLESDTLPDSCRR 117
 DB 97 LG-----MYQLFLQKE--LAE-----LREFTNQSLKVSFEKQIANPST--- 134
 QY 118 MKOAFQGVQKELQHVGPORFSGAPAMMEGSLDVAQRGKPEAQPFALHTIN--AASIP 175
 DB 135 -----PSE-----KKEPRSVAHLTGNPHSRISIP 157
 QY 176 SGSHKVTLSWYHNRGWAKISNMTLSNGKLRVQDGFYLYANICFRHHETSGSVPTDYL 235
 DB 158 -----LEWEDTYGTALISGVYKKGGLVINETGLYFVYSKYVFR-GOSCNQPLNH- 207
 QY 236 QLMVYVKTSIKIPSSHNLMKMGSTKNMGSSEHFSYINVGPFKLRAGEISIQVSNP 295
 DB 208 --KVYM--RNSKYPEDLVLMW-EKRLNYCTTGQIWAHSSYLGAVENLTSDAHUYVNISQL 262
 QY 296 SLDDPPQDATYFGAFKV 312
 DB 263 SLINFEESKTFEGLYKL 279
 RESULT 6
 FASL_HUMAN STANDARD; PRT; 281 AA.
 ID FASL_HUMAN
 AC P48023;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
 GN TNFSF6 OR APTLIG1 OR FASL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95105731.
 RA Alderson M.;
 RT "Fas ligand mediates activation-induced cell death in human T
 RL lymphocytes.";
 RL J. Exp. Med. 181:71-77(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95127560.
 RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
 RT "Human Fas ligand: gene structure, chromosomal location and species
 RT specificity.";
 RL Int. Immunol. 6:1567-1574(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Schaeuble C.E., Poehmann R., Philippsen P., Eibel H.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]

RA Shimadzu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.,
RA Matsuda I.,
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.
RX MEDLINE; 96131874.
RA Karpusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,
RA Chess L., Thomas D.,
RT "2-A crystal structure of an extracellular fragment of human CD40
ligand.";
RL Structure 3:1031-1039(1995).
RN [8]
RP 3D-STRUCTURE MODELING OF COMPLEX WITH CD40.
RX MEDLINE; 98266353.
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.,
RT "The role of polar interactions in the molecular recognition of CD40L
with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
RN [9]
RP VARIANTS HIGM1 ARG-36 AND GLY-140.
RX MEDLINE; 93156839.
RA Korthauer U., Graf D., Mages H.W., Briere F., Padayachee M.,
RA Malcolm S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.,
RA Kroczej R.A.,
RT "Defective expression of T-cell CD40 ligand causes X-linked
immunodeficiency with hyper-IgM.";
RL Nature 361:539-541(1993).
RN [10]
RP VARIANTS HIGM1 GLU-123.
RX MEDLINE; 93156840.
RA Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A.,
RA de Saint Basile G.,
RT "CD40 ligand mutations in x-linked immunodeficiency with hyper-IgM.";
RL Nature 361:541-543(1993).
RN [11]
RP VARIANTS HIGM1 PRO-155; ASP-211 AND VAL-227.
RX MEDLINE; 93174270.
RA Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A.,
RA Copeland N.G., Bedell M.A., Edelfoff S., Distche C.M.,
RA Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.,
RT "CD40 ligand gene defects responsible for X-linked hyper-IgM
syndrome.";
RL Science 259:990-993(1993).
RN [12]
RP VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144.
RX MEDLINE; 95233436.
RA Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnani D.,
RA Giliani S., Mantuano E., Fasth A., Andersson B., Zegers B.J.M.,
RA Cavagni G., Reznick I., Levy J., Zan-Bar I., Porat Y., Airol P.,
RA Plebani A., Vezzoni P., Notarangelo L.D.,
RT "Characterization of nine novel mutations in the CD40 ligand gene in
patients with X-linked hyper IgM syndrome of various ancestry.";
RL Am. J. Hum. Genet. 56:898-906(1995).
RN [13]
RP VARIANTS HIGM1 PRO-155 AND VAL-227, AND VARIANT ARG-219.
RX MEDLINE; 96133533.
RA Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,
RA Gatti R.A., Derauf D.C., Belmont J.W., Conley M.E.,
RT "A single strand conformation polymorphism study of CD40 ligand.
Efficient mutation analysis and carrier detection for X-linked hyper
IgM syndrome.";
RL J. Clin. Invest. 97:196-201(1996).
RN [14]
RP VARIANTS HIGM1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.
RX MEDLINE; 97295077.
RA Nonoyama S., Shimadzu M., Toru H., Seyama K., Nunoi H., Neubauer M.,
RA Yata J.-I., Ochi H.D.,
RT "Mutations of the CD40 ligand gene in 13 Japanese patients with
X-linked hyper-IgM syndrome.";
RL Hum. Genet. 99:624-627(1997).
CC CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.

CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
EXTRACELLULAR SOLUBLE FORM.
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
T-LYMPHOCYTES.
CC -1- DISEASE: DEFECTS IN CD40LG ARE THE CAUSE OF AN X-LINKED
IMMUNODEFICIENCY WITH HYPER-IGM (HIGM1), AN IMMUNOGLOBULIN ISOTYPE
SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM
IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES
PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE)
RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING
PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO
CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH
INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,
WITH A DEATH RATE OF ABOUT 10% BEFORE ADOLESCENCE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -1- DATABASE: NAME=CD40Lbase;
NOTE=EUROPEAN CD40L DEFECT DATABASE (MUTATION DB);
WWW="HTTP://WWW.EXPASY.CH/CD40LBASE/";
FTP="FTP://FTP.EXPASY.CH/DATABASES/CD40LBASE";
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD154 entry;
WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD154.HTM".
CC -----
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CC -----
DR EMBL; X68550; CAA48554.1; -
DR EMBL; Z15017; CAA78737.1; -
DR EMBL; X67878; CAA48077.1; -
DR EMBL; L07414; AAA35662.1; -
DR EMBL; D31797; BAA06599.1; -
DR EMBL; D31793; BAA06599.1; JOINED.
DR EMBL; D31794; BAA06599.1; JOINED.
DR EMBL; D31795; BAA06599.1; JOINED.
DR EMBL; D31796; BAA06599.1; JOINED.
DR PIR; S25684; S25684.
DR PIR; S26694; S26694.
DR PIR; S28017; S28017.
DR PIR; S28852; S28852.
DR PIR; JH0793; JH0793.
DR PDB; 1ALY; 17-SEP-97.
DR MIM; 308230; -
DR INTERPRO; IPR000478; -
DR PFAM; PF00229; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
KW Disease mutation; Polymorphism.
DR DOMAIN 1 22
DR TRANSMEM 23 46
FT FT CYTOPLASMIC (POTENTIAL).
FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT M -> R (IN HIGM1).
FT FT /FTId=VAR_007513.
FT FT A -> E (IN HIGM1).
FT FT /FTId=VAR_007514.
FT FT V -> A (IN HIGM1).
FT FT /FTId=VAR_007515.
FT FT SE -> RG (IN HIGM1).
FT FT /FTId=VAR_007516.
FT FT W -> C (IN HIGM1).
FT FT /FTId=VAR_007517.
FT FT W -> G (IN HIGM1).
FT FT /FTId=VAR_007518.
FT FT W -> R (IN HIGM1).
FT FT 140

[illegible]

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[illegible]

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RX MEDLINE; 93200072.
RA Peitsch M.C., Jongeneel C.V.;
RT "A 3-D model for the CD40 ligand predicts that it is a compact trimer
RL similar to the tumor necrosis factors.";
RN Int'l Immunol. 5:233-238(1993).
CC -!- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
CC T-LYMPHOCYTES.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
DR EMBL; X65453; CAA46448.1; -.
DR PIR; S21738; S21738.
DR PDB; 1CDA; 31-OCT-93.
DR MGD; MGI-88337; TNFSF5.
DR INTERPRO; IPR000478; -.
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR CYTOKINE; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure.
FT DOMAIN 1 22
FT TRANSMEM 23 46
FT SIGNAL-ANCHOR (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 47 260
FT EXTRACELLULAR (POTENTIAL).
FT DISULFID 177 217
FT POTENTIAL.
FT CARBOHYD 239 239
FT N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 260 AA; 29396 MW; 7E0F34F7473668B7 CRC64;

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Query Match 9.4%; Score 157; DB 1; Length 260;
Best Local Similarity 24.8%; Pred. No. 5.4e-06;
Matches 75; Conservative 51; Mismatches 105; Indels 72; Gaps 16;

QY 32 PAPSAPAPPAAASRSMFLALLGLGL-GQVVCSTALFLYFRAQMDPNRISDSTHCYR 90
DB 8 PPSRSVATGLP--ASMKTFMYLLTVLITQMTGSLVFAVYLHRRLD--KVEEE----- 56
QY 91 IRLRLE-----NAGLQDSTLESDTLDPDCRRMKQAFQAVQ-----KELQHV 134
DB 57 -VNLHEDVFVFKLRCKNGEGSLSL-----NCEMRROFEDLVKDTLNKE----- 103
QY 135 GPQRFSGAPAMMEGSLDVAQKPEAPFAHLTINAASIPSGSHKVTLSWYHGRGMAK 194
DB 104 -----EKKENSF--EMQRGDEDPQIAHVHVEA-----NSNAASVLQAKKGYTM 147
QY 195 ISNMT-LSNGK-LRYNQDGFYLYANICF-RHETSGSVPTDYQLQMLVYVVTSTK--IP 249
DB 148 KSNLVLENGKOLTVKREGLYVYVTVTFCNSNRPESSQRP-----PIVGLWLKPSIG 199
QY 250 SSHNLKMGSTKNWGSNFEHFEYSINVGFFKLRAGEEISIOVNSPSLDDPDQDATYFGA 309
DB 200 SERILLKANTHSSQOLCEQQ--SVHLGGVFELQAGASVFNVTASQVHRHVGFSFGL 257
QY 310 FKV 312
DB 258 LKL 260

RESULT 10
TNFA_HORSE
ID TNFA_HORSE STANDARD; PART; 234 AA.

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AC P29553;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92084125.
RA Su X., Morris D.D., McGraw R.A.;
RT "Cloning and characterization of gene TNF alpha encoding equine tumor
RT necrosis factor alpha.";
RL Gene 107:319-321(1991).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
DR EMBL; M64087; AAA30959.1; -.
DR PIR; JQ1344; JQ1344.
DR HSP; P01375; ITNF.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR CYTOKINE; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
KW PROPEP 1 77
KW CHAIN 78 234
KW TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 146 178
FT BY SIMILARITY.
SQ SEQUENCE 234 AA; 25469 MW; E79ACE91143DF373 CRC64;

Query Match 8.9%; Score 149; DB 1; Length 234;
Best Local Similarity 24.1%; Pred. No. 2.2e-05;
Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

QY 133 IVGPQRFSGAPAMMEGSLDVAQKQ-----PEAQFAHLTINAASIPSGSHKVTLSWY 187
DB 55 VIGPQREQLPNAFQ-SINPLAQLTRSSRTPSKPVAHVAN-----PQAEGL---QWL 106
QY 188 HDRGWAKISN-MTSLNGKLRVNDQGFYLYANICFRHETSGSVPTDYQLQMLVYVVTSTI 246
DB 107 SGRANALLANGVKLTQNLVPLDGLYLSQVLFK----GQCGPSTHVLTHHTISRLAV 162
QY 247 KIPSSHNLKMG-----GSTNWSGNSFEHFEYSINVGFFKLRAGEEISIQVSN 294
DB 163 SYPSKVNLLSAIKSPCHTESPEQAEAKPW-----YEPIYLGGVFQLEKGDQLSAEINQ 215
QY 295 PSLLD-PDQDATVFG 308

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Query Match      8.9%; Score 148.5; DB:1; Length 233;
Best Local Similarity 25.6%; Pred. NO. 2.4e-05;
Matches 50; Conservative 38; Mismatches 68; Indels 39; Gaps 11;

QY 133  IVGQR--FSGAPAMGSGWLDVAQRK---PQAQPPAHLTINAASIPSGSHKVTLSWY 187
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 55  VIGQREFFPKDPSL--SPLAQAVRSSRSTPDKPVAHVAN-----PQAEGQL---QWL 105
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 188  HDRGWAAKISN-MTSLNGKLRVNDGGFYLLYANTICFRHIHETSGSVPTDYLQI-----M 238
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Query Match      8.8%; Score 147.5; DB 1; Length 233;
Best Local Similarity 25.6%; Pred. No. 2.9e-05;
Matches 50; Conservative 38; Mismatches 66; Indels 39; Gaps 11;

QY 133 IVGPQR--FSGAPAMEGSWLDVAORGK---PEAOPFAHLTINAASIPSGSHKVTLSSHY 187
DB 55 VIGQREEFKDPKSLI--SPLAQAVRSSRTPSDKPVAVHVVAN---PQAEQGL---QWL 105
QY 188 HDRGWAKISN-MTLNKGKLRVNODGFYVLYANICFRHHETSGSVPTDYLLQL-----M 238
DB 106 NRRANALLANGVELTDNQLVPSSEGLIYISQVLEK---GQCPSNVHLLTHTSRIAV 161
QY 239 VYVK-----TSIKPSSHNLKMGKSTKWSNGSEFHFYSINVGFFKLRAGEEISIQVSN 294
DB 162 SVQTVNLLSAIKSPQRETPEGAEPKW-----YEPYILGGVFOLEKGRDLSAEINL 214
QY 295 PSLLD-PPDQATYFG 308
DB 215 PDYLDFAESGQVYFG 229

RESULT 13
TNFA_MOUSE
ID TNFA_MOUSE STANDARD; PRT: 235 AA.
AC P06804; Q62326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88224564.
RA Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.;
RT "Cloning and expression in Escherichia coli of the gene for mouse
RL tumor necrosis factor.";
RN DNA 7:193-201(1988).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85298296.
RA Pennica D., Hayflick J.S., Bringman T.S., Palladino M.A.,
RA Goeddel D.V.;
RT "Cloning and expression in Escherichia coli of the cDNA for murine
RL tumor necrosis factor.";
RN Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86149365.
RA Capt D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,
RA Cerami A.;
RT "Identification of a common nucleotide sequence in the
RL 3'-untranslated region of mRNA molecules specifying inflammatory
RT mediators.";
RN Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85242112.
RA Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,
RA Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,
RA Ruyschaert M.-R., Fiers W.;
RT "Molecular cloning of mouse tumour necrosis factor cDNA and its
RL eukaryotic expression.";
RN Nucleic Acids Res. 13:4417-4429(1985).
[5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87298639.
RA Shakhov A.N., Nedospasov S.A.;
RT "Molecular cloning of genes coding for tumor necrosis factor.
RT Complete nucleotide sequence of the genome copy of TNF-alpha in

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mice.";
RL Bioorg. Khim. 13:701-705(1987).
[6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88067722.
RA Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;
RT "Nucleotide sequence of the murine TNF locus, including the TNF-alpha
RT (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";
RN Nucleic Acids Res. 15:9083-9084(1987).
[7]
RP SEQUENCE FROM N.A.
RX STRAIN-CTS, AND NOD;
RX MEDLINE; 96013654.
RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,
RA Takekawa K., Ogihara T.;
RT "Identification of a new susceptibility locus for insulin-dependent
RT diabetes mellitus by ancestral haplotype congenic mapping.";
RL J. Clin. Invest. 96:1936-1942(1995).
[8]
RP SEQUENCE OF 80-99.
RX MEDLINE; 91097531.
RA Sherry B., Juc D.-M., Zentella A., Cerami A.;
RT "Characterization of high molecular weight glycosylated forms of
RT murine tumor necrosis factor.";
RL Biochem. Biophys. Res. Commun. 173:1072-1078(1990).
[9]
RP SEQUENCE OF 70-87.
RX MEDLINE; 89380231.
RA Cseh K., Beutler B.;
RT "Alternative cleavage of the cachectin/tumor necrosis factor
RT propeptide results in a larger, inactive form of secreted protein.";
RL J. Biol. Chem. 264:16256-16260(1989).
[10]
RP IDENTIFICATION OF MEMBRANE-BOUND FORM.
RX MEDLINE; 88165056.
RA Kriegl M., Perez X., Defay K., Albert I., Lu S.D.;
RT "A novel form of TNF/cachectin is a cell surface cytotoxic
RT transmembrane protein: ramifications for the complex physiology of
RT TNF.";
RL Cell 53:45-53(1988).
[11]
RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.
RX MEDLINE; 99190964.
RA Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;
RT "The structure of mouse tumour-necrosis factor at 1.4 A resolution:
RT towards modulation of its selectivity and trimerization.";
RL Acta Crystallogr. D 55:772-778(1999).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
CC EMBL; U06950; AAA18594.1; -
DR

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DR EMBL; M13049; AAA40457.1; -
DR EMBL; M11731; AAA40458.1; -
DR EMBL; Y00467; CAA68530.1; -
DR EMBL; X02611; CAA26457.1; -
DR EMBL; M20155; AAA40462.1; ALT_SEQ.
DR EMBL; M38296; AAA40459.1; -
DR EMBL; D84196; BAA19512.1; -
DR EMBL; D84194; BAA19512.1; JOINED.
DR EMBL; D84195; BAA19512.1; JOINED.
DR EMBL; D84199; BAA19513.1; -
DR EMBL; D84197; BAA19513.1; JOINED.
DR EMBL; D84198; BAA19513.1; JOINED.
DR PIR; A23127; QWMSN.
DR PIR; A22908; A22908.
DR PIR; A25164; A25164.
DR PIR; A27303; A27303.
DR PIR; A34251; A34251.
DR PIR; S03791; S03791.
DR PDB; 2TNF; 12-OCT-99.
DR MGD; MGI:104798; TNF.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine, Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
KW 3D-structure.
FT PROPEP 1 79
FT CHAIN 80 235 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 148 179
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .).
FT CONFLICT 231 231 G -> R (IN REF. 3 AND 4).
FT SEQUENCE 235 AA; 25895 MW; 16DD2A9676D68C5D CRC64;

Query Match 8.7%; Score 146.5; DB 1; Length 235;
Best Local Similarity 25.6%; Pred. No. 3.5e-05;
Matches 51; Conservative 36; Mismatches 67; Indels 45; Gaps 11;

QY 133 IVGPQR---SCAP---AMMECSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLS- 184
DB 55 VIGPQREKFPNGPLPLISSMAQTLTRSSQNSSD-KPAHVAVN-----HQVEQL 105

QY 185 SWYHGRGAKISN-MTLSNGKLRVNDGFFLYLANICFRHHTSGSVPTDYQLQMLWYVVK 243
DB 106 EWLSQLRANALLANGMDLKNQLVVPADGLYLVISQVLFK-----GQCCPDYV-LLTHTVS 159

QY 244 -----TSIKIPSSHNLKMGSGTKNWSGNSEHFYSINVGFFKLRAGEEISI 290
DB 160 REAISYOEKVNLLSAVSKPCPKDTPGAEALKPW-----YEPYILGGVFOLEKGDQLSA 212

QY 291 QVSNPSLLD-PQDATYFG 308
DB 213 EYNLPKYLDFAESGGVYFG 231

RESULT 14
TNFA_PAPHU
ID TNFA_PAPHU STANDARD; PRT; 233 AA.
AC 077510;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Papio hamadryas ursinus (Chacma baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
RN [1]

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SEQUENCE FROM N.A.
RX MEDLINE: 98147379.
RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
  alpha.";
RL Mol. Immunol. 34:1041-1042(1997).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
  WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
  CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
  CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
  OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
  CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
  CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
  EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
  PROTEOLYTIC PROCESSING.
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
  CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
  AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
EMBL; AF019963; AAC31675.1; -.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 76 BY SIMILARITY.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 145 177 BY SIMILARITY.
FT SEQUENCE 233 AA; 25658 MW; B9403255058D4A03 CRC64;

Query Match 8.6%; Score 143.5; DB 1; Length 233;
Best Local Similarity 25.1%; Pred. No. 6.1e-05;
Matches 49; Conservative 38; Mismatches 69; Indels 39; Gaps 11;

QY 133 IVGPQR--FSGAPAMMECSWLDVAQRGK---PEAQPFAHLTINAASIPSGSHKVTLSWY 187
DB 55 VIGPQREKFPKPSLI--SPLAQAVRSSRTPSDKPVVHVAN---PQAEQL---QWL 105

QY 188 HDRGWAKISN-MTLSNGKLRVNDGFFLYLANICFRHHTSGSVPTDYQLQ-----M 238
DB 106 NRRANALLANGVELTDNQLVVPSEGLYLIYSQVLFK---GQCCPSNHVLLTHTSRIAV 161

QY 239 VYVVK-----TSIKIPSSHNLKMGSGTKNWSGNSEHFYSINVGFFKLRAGEEISQVSN 294
DB 162 SYQTKVNLLSAIKSPQRETPEGAEPKW-----YEPYILGGVFOLEKGRLSAEINL 214

QY 295 PSLLD-PQDATYFG 308
DB 215 PDYLDFAESGGVYFG 229

RESULT 15
TNFA_PAPSP
ID TNFA_PAPSP STANDARD; PRT; 233 AA.
AC P33620;
DT 01-FEB-1994 (Rel. 28, Created)

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Db 215 PDYLDFAESGVVFG 229

Search completed: December 29, 2000, 09:04:18
Job time: 48342 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 28, 2000, 19:38:02 ; Search time 601.22 Seconds
(without alignments)
49.077 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYLRSSEMGs.....LLDPDQATYGFAPKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL14.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mmc.*
- 8: sp_organalle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	11 Q35235	O35235 mus musculus
2	1646.5	98.3	313	11 Q9R1Y0	Q9r1y0 mus musculus
3	1417.5	84.6	317	4 Q14788	Q14788 homo sapien
4	164	9.8	260	6 Q97605	Q97605 felis silve
5	154	9.2	260	6 Q97626	Q97626 canis famli
6	149	8.9	234	6 Q9RTJ3	Q9rtj3 equus caball
7	148	8.8	232	11 Q35853	Q35853 mus musculus
8	146.5	8.7	239	11 Q9QYH9	Q9qyh9 mus musculus
9	145	8.7	260	11 Q9Z2V2	Q9z2v2 rattus norv
10	145	8.7	260	11 Q9R254	Q9r254 rattus norv
11	142	8.5	232	4 Q9UIV3	Q9uiv3 homo sapien
12	140	8.4	174	4 Q9S150	Q9s150 homo sapien
13	139	8.3	234	6 Q28320	Q28320 capra hircu
14	134.5	8.0	240	4 Q43557	Q43557 homo sapien
15	133.5	8.0	233	6 Q18779	Q18779 bos taurus
16	133	7.9	157	4 Q43647	Q43647 homo sapien
17	132	7.9	149	6 Q97543	Q97543 aotus nancy
18	131	7.8	149	6 Q97538	Q97538 aotus vocif
19	131	7.8	149	6 Q9TTG8	Q9ttg8 aotus nigri

20	130.5	7.8	240	4	Q75476	O75476 homo sapien
21	130	7.8	216	11	Q70332	O70332 mesocricetu
22	126.5	7.6	250	6	Q9XT47	Q9xt47 macropus eu
23	123.5	7.4	138	6	Q9TTG7	Q9ttg7 aotus lemur
24	120.5	7.2	150	6	Q9TSV8	Q9tsv8 sus scrofa
25	109	6.5	201	6	Q9XT48	Q9xt48 macropus eu
26	103	6.1	3848	5	Q76737	O76737 dictyostelli
27	102.5	6.1	225	11	Q54907	Q54907 mus musculu
28	102	6.1	169	11	Q9WV90	Q9wv90 marmota mon
29	99.5	5.9	558	5	Q45692	Q45692 caenorhabdi
30	97	5.8	325	5	Q9V5G2	Q9v5g2 drosophila
31	96	5.7	1486	13	Q91717	Q91717 xenopus lae
32	95	5.7	1012	4	Q9UEF7	Q9uef7 homo sapien
33	94	5.6	891	1	Q93635	Q93635 thermococcu
34	93	5.6	93	6	Q9TTJ2	Q9ttj2 bos taurus
35	92	5.5	294	2	Q53921	Q53921 synechococc
36	92	5.5	549	4	Q9Y4F0	Q9y4f0 homo sapien
37	92	5.5	785	5	Q9XU57	Q9xus7 caenorhabdi
38	92	5.5	1012	4	Q9UEI9	Q9uei9 homo sapien
39	91.5	5.5	205	4	Q9UKS8	Q9uks8 homo sapien
40	91	5.4	616	4	Q9UBP0	Q9ubp0 homo sapien
41	90.5	5.4	750	10	Q9Z008	Q9zq08 arabidopsis
42	90	5.4	355	5	Q9VG08	Q9vgq8 drosophila
43	90	5.4	556	12	Q9WNB6	Q9wnb6 caprine art
44	90	5.4	3011	12	Q03463	Q03463 hepatitis c
45	88	5.3	347	2	Q9RR94	Q9rr94 deinococcus

ALIGNMENTS

RESULT 1

O35235 PRELIMINARY; PRT; 316 AA.

AC O35235: Q35306;

DT 01-JAN-1998 (TREMREL. 05, Created)

DT 01-JAN-1998 (TREMREL. 05, Last sequence update)

DT 01-MAY-2000 (TREMREL. 13, Last annotation update)

DE TNF-RELATED ACTIVATION-INDUCED CYTOKINE (RANKL) (TRANCE) (OPGL)

DE (OSTEOPROTEGERIN LIGAND) (TUMOR NECROSIS FACTOR LIGAND) (OSTEOCLAST

DE DIFFERENTIATION FACTOR) (ODF).

GN TNFSF11 OR RANKL OR TRANCE OR OPGL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[[1]]

RP SEQUENCE FROM N.A.

RC TISSUE=HYBRIDOMA;

RX MEDLINE; 97460112.

RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,

RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,

RA Choi Y.;

RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family

RT that activates c-Jun N-terminal kinase in T cells.";

RL J. Biol. Chem. 272:25190-25194(1997).

[[2]]

RP SEQUENCE FROM N.A.

RC TISSUE=BONE MARROW;

RX MEDLINE; 98227661.

RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,

RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,

RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,

RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,

RA Boyle W.J.;

RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast

RT differentiation and activation.";

RL Cell 93:165-176(1998).

[[3]]

RP SEQUENCE FROM N.A.

RC TISSUE=BONE MARROW STROMA;

RX MEDLINE; 98188248.

RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,

RA Mochizuki S.-H., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,

RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT "Osteoclast differentiation factor is a ligand for
RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RL to TRANCE/RANKL.";
RN Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RP (4)
RC SEQUENCE FROM N.A.
RX TISSUE-THYMIC LYMPHOMA;
RX MEDLINE; 98032977.
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
CC -!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC PROLIFERATION.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: HIGHER LEVELS IN THE BONE MARROW AND STROMAL
CC CELLS THAN SPLEEN, THYMUS AND LYMPH NODE.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
DR EMBL; AF053713; AAC40113.1; -.
DR EMBL; AF013170; AAC71061.1; -.
DR EMBL; AB008426; BAA25425.1; -.
DR EMBL; AF019048; AAB86812.1; -.
DR MGD; MGI:1100089; Tnfsf11.
DR INTERPRO; IPR000478; -.
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 99 99 G -> D (IN REF. 4).
SQ SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;

Query Match 100.0%; Score 1675; DB 11; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.5e-147;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYCKYLRSEEMSGSGVPGHPGHPAPAPAPPAPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYCKYLRSEEMSGSGVPGHPGHPAPAPAPPAPPAASRSMFLALLGLGLGQ 60

Qy 61 VVCSIALFLYFRAQMDPNRISEDSHCHFYRLRLHENAGLQDSTLESDTLPSDCRRMKQ 120
Db 61 VVCSIALFLYFRAQMDPNRISEDSHCHFYRLRLHENAGLQDSTLESDTLPSDCRRMKQ 120

Qy 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQGRKPEAQPFAPHAHTINAASIPSGSHK 180
Db 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQGRKPEAQPFAPHAHTINAASIPSGSHK 180

Qy 181 VTLSSWYHDSRGWAKISNTLSNGKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQVMY 240
Db 181 VTLSSWYHDSRGWAKISNTLSNGKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQVMY 240

Qy 241 VVKTSIKIPSSHNLKMGSTKNWNSGFHYISINVGGFFKLAGEEISIQVSNPSLLDP 300
Db 241 VVKTSIKIPSSHNLKMGSTKNWNSGFHYISINVGGFFKLAGEEISIQVSNPSLLDP 300

Qy 301 DQDATYFGAFKVDID 316
Db 301 DQDATYFGAFKVDID 316

RESULT 2

Q9RLY0 Q9RLY0 PRELIMINARY; PRT; 313 AA.
ID Q9RLY0;
AC Q9RLY0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE OSTEOCLAST DIFFERENTIATION FACTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA Ueda M., Higashio K.;
RT "Cloning and characterization of the gene encoding mouse osteoclast
RT differentiation factor.";
RL Gene 230:121-127(1999).
DR EMBL; AB022039; BAA36970.1; -.
DR EMBL; AB022036; BAA36970.1; JOINED.
DR EMBL; AB022037; BAA36970.1; JOINED.
DR EMBL; AB022038; BAA36970.1; JOINED.
DR INTERPRO; IPR000478; -.
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 313 AA; 34719 MW; 37D530B8BFC2842E CRC64;

Query Match 98.3%; Score 1646.5; DB 11; Length 313;
Best Local Similarity 99.1%; Pred. No. 6.4e-145;
Matches 313; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MRRASRDYCKYLRSEEMSGSGVPGHPGHPAPAPAPPAPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYCKYLRSEEMSGSGVPGHPGHPAPAPAPPAPPAASRSMFLALLGLGLGQ 60

Qy 61 VVCSIALFLYFRAQMDPNRISEDSHCHFYRLRLHENAGLQDSTLESDTLPSDCRRMKQ 120
Db 61 VVCSIALFLYFRAQMDPNRISEDSHCHFYRLRLHENAGLQDSTLESDTLPSDCRRMKQ 120

Qy 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQGRKPEAQPFAPHAHTINAASIPSGSHK 180
Db 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQGRKPEAQPFAPHAHTINAASIPSGSHK 177

Qy 181 VTLSSWYHDSRGWAKISNTLSNGKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQVMY 240
Db 181 VTLSSWYHDSRGWAKISNTLSNGKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQVMY 237

Qy 241 VVKTSIKIPSSHNLKMGSTKNWNSGFHYISINVGGFFKLAGEEISIQVSNPSLLDP 300
Db 238 VVKTSIKIPSSHNLKMGSTKNWNSGFHYISINVGGFFKLAGEEISIQVSNPSLLDP 297

Qy 301 DQDATYFGAFKVDID 316
Db 298 DQDATYFGAFKVDID 313

RESULT 3
O14788
ID O14788 PRELIMINARY; PRT; 317 AA.
AC O14788; O14723;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE TNF-RELATED ACTIVATION-INDUCED CYTOKINE (RANKL) (TRANCE) (OPGL)
DE (OSTEOPROTEGERIN LIGAND) (TUMOR NECROSIS FACTOR LIGAND).
OS TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW, AND PERIPHERAL BLOOD;


```
GN CD40L.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RA Hosie M.H., Willett B.J.;
RT "Adjuvant properties of canine CD40L.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF086711; AAD04375.1; -.
DR HSSP; P29965; ITALY.
DR INTERPRO; IPR000478; -.
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 260 AA; 28688 MW; 604F69A1E98EB70 CRC64;

Query Match 9.2%; Score 154; DB 6; Length 260;
Best Local Similarity 24.7%; Pred. No. 1.6e-06;
Matches 72; Conservative 54; Mismatches 114; Indels 52; Gaps 17;

QY 33 APSAPAPPPAASRSMELALLGLGQVVCISALF-LYFRAQMDPNRISEDSHCF--Y 89
DB 9 APRSVATGPP--VSMKIFMYLLTVLITQMIGSALFAYLYHRRLDK---IEDERNLYEDF 63
QY 90 RLRLHENAGLDQSTLESEDLPDSCRRMKQAFQAVOKELQHIIVGPORFSGAPAMMEGS 149
DB 64 VPMKTLQCNKGEGLSLL-----NCEIKSQFE-AFLKEIM-LNEMKEENIAM---- 112
QY 150 WLDVAQRGKPEAQPFALHTINAASIPSGSHKVTLSWYHDSRWAKISN--MTLSNGK-LR 206
DB 113 -----QKGDQDPRIAAHVISEASSNPA-----SVLRW-APKGYITISNLVSLKNGKQLA 161
QY 207 VNQDGFYLYANICF-RHETSGSVPTDYQLQMLVYVVKTSIKIPSSH--LMKGGSTKNW 263
DB 162 VKRQGLYLYYAQVTCFSNRAASSQAP-----FVASICLHSPGSTERVLLRAASRGS 213
QY 264 S---GNSEFHFYINVGGFKLRAGEEISIOVNSPSLLDPDQDATYFGAFKV 312
DB 214 SKPCGQQ-----SIHLGGVFELHPGASVFNVTDFSQVSHGIGFTSFGLLKL 260

RESULT 6
Q9TTJ3
ID Q9TTJ3 PRELIMINARY; PRT; 234 AA.
AC Q9TTJ3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TUMOR NECROSIS FACTOR-ALPHA.
GN TNFA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RA Ishida N., Sato F., Hasegawa T.;
RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035735; BAA88349.1; -.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR INTERPRO; IPR002960; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PRINTS; PR01236; TNFBETA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;

us-08-989-362-2.rspt

Query Match 8.9%; Score 149; DB 6; Length 234;
Best Local Similarity 24.1%; Pred. No. 4.1e-06;
Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

QY 133 IVGPORFSGAPAMMEGSWLDVAQRGK-----PEAQPFALHTINAASIPSGSHKVTLSWY 187
DB 55 VIGPQREQLPNAFQ-SINLAQTLRSSRTPSDKPAHVAVN----PQAEGLQ---QWL 106
QY 188 HDRGWAKISN-MTLSNGKLRVNDGFFLYLYANICFRHETSGSVPTDYQLQMLVYVVKTSI 246
DB 107 SGRANALLANGVKLTNDQLVVPDGLYLYISQVLFK-----GQGPCSTHVLTHHTISRLAV 162
QY 247 KIPSSHNLMKG-----GSTKNWGSNSEFHFYSINVGGFKLRAGEEISIOVSN 294
DB 163 SYPSKVNLLSAIKSLANTESPEQAEPW-----YEPIYLGGVFQLEKGDQLSAEINQ 215
QY 295 PSLLD-PDQDATYFG 308
DB 216 PNYLDFAESGVYFG 230

RESULT 7
Q35853
ID Q35853 PRELIMINARY; PRT; 232 AA.
AC Q35853;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR ALPHA.
GN TNFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE; 97246744.
RA Iraqi F., Teale A.;
RT "Cloning and sequencing of the tnfa genes of three inbred mouse strains.";
RL Immunogenetics 45:459-461(1997).
DR EMBL; U68414; AAB65593.1; -.
DR HSSP; P01375; 4TSV.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 232 AA; 25513 MW; 2ED6DA8E0DCAADD8 CRC64;

us-08-989-362-2.rspt

Query Match 8.8%; Score 148; DB 11; Length 232;
Best Local Similarity 24.6%; Pred. No. 5e-06;
Matches 48; Conservative 34; Mismatches 73; Indels 40; Gaps 9;

QY 133 IVGPQR---FSGAPAMMEGSWLDVAQRGKPEAQPFALHTINAASIPSGSHKVTLS-SWYH 188
DB 55 VIGPQRDEKPNGLPLTSSNAQTLSSSQNSDKPAHVAVN-----HQVEGLEWLS 106
QY 189 DRGWAKISN-MTLSNGKLRVNDGFFLYLYANICFRHETSGSVPTDYQLQMLVYVVK---- 243
DB 107 QRANALLANGMDKDNQLVVPADGLYLYVSVLFK-----GQGPCDYV-LLTHVTSREAI 160
QY 244 -----TSIKPSHNLMKGGSTKNWGSNSEFHFYSINVGGFKLRAGEEISIOVSN 294
DB 161 SYOEKVNLLSAVSPCKPTEGAELPW-----YEPIYLGGVFQLEKGDQLSAEYNL 213
QY 295 PSLLD-PDQDATYFG 308
DB 214 PNYLDFAESGVYFG 228
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Db 160 VSYQTKVNLSSAIKSPCQRETPEGAKEPW-----YEPIYLGGVFQLEKGDRLSAEIN 212

Qy 294 NPSLLD-PDQDATYFG 308

Db 213 RPDYLDFAESGQVYFG 228

RESULT 12

O95150

ID O95150 PRELIMINARY; PRT; 174 AA.

AC O95150;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE VASCULAR ENDOTHELIAL CELL GROWTH INHIBITOR.

GN VEG1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-VASCULAR ENDOTHELIAL;

RA Yu G.-L., Zhai Y., Ni J., Iruela-Arispe L., Huang W.-Q., Xing L.,

RA Lu J., Kozak D., Jiang G.-W., Rojas L., Janat M.F., Buergerin M.,

RA Gentz S., Lippman M.E., Aggarwal B.B., Ruben S., Gentz R., Li L.-Y.,

RA Yu G.-L.;

RT "A Novel Endothelial Cell-Specific Negative Regulator of

RT Angiogenesis.";

RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF039390; AAD08783.1; -.

DR HSSP; P01375; 1A8M.

DR INTERPRO; IPR000478; -.

DR PFAM; PF00229; TNF; 1.

DR PRINTS; PR01234; TNECROSISFCT.

DR PROSITE; PS50049; TNF_2; 1.

SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;

Query Match 8.4%; Score 140; DB 4; Length 174;

Best Local Similarity 28.3%; Pred. No. 1.9e-05;

Matches 39; Conservative 24; Mismatches 55; Indels 20; Gaps 5;

Qy 186 WYDRGWAKISN-WTLSNGKLVNQDGGFYLYANICFRHH-----PTDYQLQM 238

Db 42 WEHELGLAFTKRMNMYTNKFLIPESGDYFYISQVTFRCMTSECSIRQAGRPKPDST 101

Qy 239 VYVVKTSIKIPSSNLMKGGST----KNWSONSEFHYSINVGFFKLRAGEEISIQVS 293

Db 102 VVITKVDYSPEPTQLMGTSKVCVGSNW-----FQPIYLGAMFSLQEGDKLMNVVS 154

Qy 294 NPSLLD-PDQDATYFGAF 310

Db 155 DISLVDYTKEDKTFEGAF 172

RESULT 13

ID Q28320 PRELIMINARY; PRT; 234 AA.

AC Q28320;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE TNF-ALPHA.

OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Capra.

RN [1]

RP SEQUENCE FROM N.A.

RA Takakura H., Mori Y., Tatsumi M.;

RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in

RT E.coli and insect cells.";

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; D86587; BAA13130.1; -.

DR HSSP; P01375; 4TSV.

DR INTERPRO; IPR000478; -.

DR INTERPRO; IPR002959; -.

DR PFAM; PF00229; TNF; 1.

DR PRINTS; PR01234; TNECROSISFCT.

DR PRINTS; PR01235; TNFALPHA.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS50049; TNF_2; 1.

SQ SEQUENCE 234 AA; 25519 MW; 9768E33BBABB041 CRC64;

Query Match 8.3%; Score 139; DB 6; Length 234;

Best Local Similarity 25.7%; Pred. No. 3.9e-05;

Matches 49; Conservative 30; Mismatches 82; Indels 30; Gaps 9;

Qy 133 IVGPQRFSGAPAMME-CSWLDDVAQRKPEA---OPFAHLTINAASIPSGSHKVTLSWYH 188

Db 55 VIGPQREEQSPAGPSFNRPLVQTLRSSQASSNRPVAHVANI-----SAPQLRWGDSYA 110

Qy 189 DRGWAKISNMTLSNGKLVNQDGGFYLYANICFRHH-----ETSGSVPTDYQLQM 238

Db 111 NA--LRANGVELKDNQLVWPTDGLYLSQVLFGRGHCPSPTPLFTHTISRIASVY-QTK 167

Qy 239 VYVVKTSIKIPSSNLMKGGSTKNWSONSEFHYSINVGFFKLRAGEEISIQVNSPLL 298

Db 168 VNTL-SAIKSPCHRETPEGAKEPW-----YEPIYQGGVFQLEKGDRLSAEINQPEYL 219

Qy 299 D-PDQDATYFG 308

Db 220 DYAESGVYEG 230

RESULT 14

O43557 PRELIMINARY; PRT; 240 AA.

AC O43557;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE TUMOR NECROSIS FACTOR SUPERFAMILY MEMBER LIGHT.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 98122340.

RA Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,

RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,

RA Ware C.F.;

RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are

RT ligands for herpesvirus entry mediator.";

RL Immunity 8:21-30(1998).

DR EMBL; AF036581; AAC39563.1; -.

DR HSSP; P01375; 4TSV.

DR INTERPRO; IPR000478; -.

DR PFAM; PF00229; TNF; 1.

DR PROSITE; PS50049; TNF_2; 1.

SQ SEQUENCE 240 AA; 26351 MW; 49D0BF67E1390B39 CRC64;

Query Match 8.0%; Score 134.5; DB 4; Length 240;

Best Local Similarity 28.5%; Pred. No. 9.3e-05;

Matches 59; Conservative 30; Mismatches 85; Indels 33; Gaps 12;

Qy 121 AFOGAVQKELQHVGPQ--RFSGAPAMMEGSLWDVAQ-RGKPEAQPFHAHLTINAASIPSG 177

Db 52 AVQGWFLQLLHWRLGEMVTRLPDGPAA--GSWEQLIERRSHEVNPAAHLT-GANSSLTG 107

Qy 178 SHKVTLSWYHDRGWAKISNMTLSNGKLVNQDGGFYLYANICFRHHETSG-SVPTDYQLQ 236

Db 108 SGGPLL--WETQLGLAFLRGLSYHDGALVVTKAGYYIYSKV-----QLGGVGCPGLIAS 160


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Qy 237 LMVY-VVKTSIKIPSHNLMKG-----GSKNWSGNSEFHYSINVGGFFKLRAGE 286
Db 161 TITHCLYKRTPRYPELELLVYQQSPCCGRATSSSRVW-WDSF-----LCGVVHLEAGE 213

Qy 287 EISTQVSNPSLLD-PDQDATYFGAFKV 312
Db 214 EWVVRVLDRLVRLDRDGRSYFGAFMV 240

RESULT 15
O18779
ID O18779 PRELIMINARY; PRT: 233 AA.
AC O18779;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR ALPHA.
GN TNFA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=N'DAMA;
RA Iraqi F.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF011926; AAB84086.1; -.
DR HSP; P01375; 4TSV.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNFCROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
SQ SEQUENCE 233 AA; 25395 MW; 8D8729025DE516B0 CRC64;

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Query Match      8.0%; Score 133.5; DB 6; Length 233;
Best Local Similarity 25.8%; Pred. No. 0.00011;
Matches 51; Conservative 30; Mismatches 72; Indels 45; Gaps 11;

Qy 133 IVGPQR--FSGAPAMMEGSLDVAQRKPEA---QPFAHLTINAASIPSGSHKVTLSWY 187
Db 55 VIGQRESPGGPSI--NSPLVQTLRSSQASSNKPVAHVAD-----INSPG 100

Qy 188 HDRGWAKISNMTLSNG-KLRVNO-----DGFYYLYANICFRHH-----ETSGSVP 231
Db 101 QLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFERQGCPTPLFLTHTISRIA 160

Qy 232 TDYLQLMVYVVKTSIKIPSHNLMKGSKTKNWSGNSEFHYSINVGGFFKLRAGEISIO 291
Db 161 VSY-QTKVNIL-SAIKSPCHRETPWEAKPW-----YEFIYGGGVFQLEKGRLSAE 211

Qy 292 VSNPSLLD-PDQDATYFG 308
Db 212 INLPDYLDYAESGGVYFG 229

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Search completed: December 29, 2000, 09:00:15
Job time: 48133 sec

OM of: US-08-989-362-2 to: EST:* out_format : pfs

Date: Dec 29, 2000 11:57 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-MODEL=frame_model;
-MODEL=frame_model;
-Q/-Cgnto_1/USPTO_Spool/US08989362/runat_28122000_095657_24313/app_query.fasta_1.377
-DB=EST -QFWT=fastap -SUFFIX=first -GAPOF=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOF=4.500
-QGAPEXT=0.050 -XGAPOF=10.000 -XGAPEXT=0.500 -FGAPOF=6.000
-QGAPEXT=7.000 -YGAPOF=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFWT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US08989362.@CGN1_1_2105 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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Search information block:

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Query: US-08-989-362-2
Query length: 316
Database: EST:*
Database sequences: 7189864
Database length: 1203564053
Search time (sec): 10166.130000
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score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
gb_gss12:AQ827122	-	622.10	1.1e-25	524	! AQ827122 HS_5256_B2_C09_T7A RPO
gb_gss12:AQ827168	-	514.68	1.1e-19	529	! AQ827168 HS_5256_B2_C09_T7A RPO
gb_est33:BE042463	-	362.44	3.2e-11	618	! BE042463 ho22c06.x1 NCI_CGAP_Cc
gb_est33:AW949689	-	351.39	1.3e-11	683	! AW949689 EST361759 MAGE resequ
gb_est25:AW945165	+	350.86	1.4e-10	718	! AW945165 EST361358 MAGE resequ
gb_gss11:AW817650	+	350.09	1.6e-10	413	! AW817650 HS_5265_B1_D03_SP6E RPO
gb_est20:AW104819	+	331.40	1.7e-09	585	! AW104819 xd57b10.x1 NCI_CGAP_Ov
gb_est32:BE000955	+	320.25	7.1e-09	652	! BE000955 RC0-BN0121-210300-031-
gb_est5:AA687481	+	260.10	1.6e-05	454	! AA687481 ns58e08.r1 NCI_CGAP_Pt
gb_est23:AW637373	+	249.17	6.5e-05	456	! AW637373 bl57h07.w1 Blackshear/
gb_est20:AW191932	+	248.19	7.4e-05	502	! AW191932 xl77d01.x1 NCI_CGAP_Pa
gb_est8:AI095853	-	246.42	9.3e-05	468	! AI095853 qb26d04.x1 Soares_Preq
gb_est3:AA298009	+	249.64	6.1e-05	320	! AA298009 EST113646 t-cell lymph
gb_est11:AI626285	+	237.08	0.0003	218	! AI626285 fc12f06.y1 zebrafish W
gb_est32:BE000089	+	213.41	0.0064	675	! BE000089 MR0-BN0070-200400-015-
gb_est38:R31020	+	232.00	0.0026	185	! R31020 yb60h08.r1 Soares placen
gb_est24:AW838386	-	207.59	0.0135	524	! AW838386 QV2-LT0053-020400-119-
gb_est12:AI660244	-	204.65	0.0196	556	! AI660244 we68h03.x1 Soares_Diec
gb_est4:AA494493	-	202.86	0.0247	563	! AA494493 ne38f03.s1 NCI_CGAP_Cc
gb_est37:HA4565	+	200.46	0.0336	477	! HA4565 yo75h09.r1 Soares breast
gb_est12:AI657160	+	196.66	0.0547	583	! AI657160 tt84c11.x1 NCI_CGAP_Pt
gb_est7:AA877776	-	195.40	0.0643	607	! AA877776 nr06g06.s1 NCI_CGAP_Cc
gb_est12:AI769552	-	194.46	0.0725	613	! AI769552 wj24d04.x1 NCI_CGAP_K1
gb_est19:AW044527	-	193.28	0.0844	586	! AW044527 wy73b10.x1 Soares_NSF
gb_est10:AI468176	-	189.43	0.1216	443	! AI468176 tg56b08.x1 NCI_CGAP_Pt
gb_est4:AA534754	-	189.96	0.1291	463	! AA534754 nf77e09.s1 NCI_CGAP_Cc
gb_est11:AI798802	-	185.93	0.2165	676	! AI798802 we92h03.x1 Soares_NFL
gb_est11:AI524976	-	188.41	0.1575	458	! AI524976 promna-2.E01.r bvtumc
gb_est35:BE457735	-	182.27	0.3466	597	! BE457735 us96e01.x1 Soares_thym
gb_est37:HS4629	-	182.91	0.3189	380	! HS4629 yq1a11.s1 Soares fetal
gb_est25:AW978651	-	177.69	0.6235	621	! AW978651 EST390760 MAGE resequ
gb_est8:AI091048	-	180.05	0.4606	460	! AI091048 qa53b04.s1 Soares_NHn
gb_est22:CN5026DP	-	169.44	1.80	986	! AI183238 Tetraodon nigroviridis
gb_est40:Z36726	+	178.48	0.5634	390	! Z36726 HHEA474M Atrium cDNA lib
gb_est20:AW188005	+	174.86	0.8962	548	! AW188005 xj91c03.x1 Soares_NFL
gb_est2:AA291356	+	175.86	0.7876	461	! AA291356 zt44c07.r1 Soares oval
gb_est7:HA43566	+	176.73	0.7047	393	! HA43566 yoc4h10.r1 Soares breast
gb_est8:AI026064	+	174.46	0.9433	450	! AI026064 ow19d06.s1 Soares para
gb_est14:AI982044	+	170.74	1.52	638	! AI982044 pat.pk0072.c9.f chick
gb_est19:AW253279	+	170.30	1.61	665	! AI253279 ESTRB0004 SuperScript
gb_est19:AW025893	-	169.47	1.79	665	! AW025893 ww71d09.x1 Soares_thym

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gb_est23:AW607607 + 109.00 175.78 0.7965 340 ! AW607607 MR3-HT0487-290100-1
gb_est37:HA4567 + 106.00 167.78 2.22 451 ! HA4567 yo75h10.r1 Soares bre
gb_est37:HA4772 + 105.00 166.52 2.61 434 ! HA4772 yp20e12.r1 Soares bre
gb_est10:AI410040 - 103.00 162.46 4.39 465 ! AI410040 EST238333 Normalize
seq_name: gb_gss12:AQ827122
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seq_documentation_block: 524 bp DNA GSS 27-AUG-1999
LOCUS AQ827122
DEFINITION HS_5256_B2_C09_T7A RPO-11 Human Male BAC Library Homo sapiens
genomic clone Plate=832 Col=18 Row=F, DNA sequence.
ACCESSION AQ827122
VERSION AQ827122.1 GI:5793184
KEYWORDS GSS.
SOURCE human.
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```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 524)
```

```
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
```

```
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
```

```
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
```

```
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
```

```
Email: jwallaceu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 832 row: F column: 18
Seq primer: T7
Class: BAC ends
High quality sequence stop: 524.
Location/Qualifiers
1..524
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"
BASE COUNT 154 a 116 c 99 g 151 t
ORIGIN
```

```
FEATURES
source
```

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alignment_scores:
Quality: 380.00 Length: 90
Ratio: 4.578 Gaps: 0
Percent Similarity: 92.222 Percent Identity: 81.111
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alignment_block:
US-08-989-362-2 x AQ827122/rev ..
Align seg 1/1 to reverse of: AQ827122 from: 1 to: 524
```

```
227 SerGlySerValProThrAspTyrLeuGlnLeuMetValTyrValVally 243
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
517 TCAGAAGACCTAGCTACAGAGTATCTTCACATAATGTCGTACGTAC 468
```

```

243| sThrSerIleLysIleProSerSerHisAsnLeuMetLysGlyGlySerT 260
    | |||||
467| ACCAGCATCAGATCCCAAGTTCTCATACCTTGATGAAGGAGGAAGCA 418
    | |||||
260| hrLysAsnTrpSerGlyAsnSerGluPheHisPheTyrSerIleAsnVal 276
    | |||||
417| CTAGTATTGGTCAGGAATATGATTCATTTTATTCATTAACGTT 368
    | |||||
277| GlyGlyPhePheLysLeuArgAlaGlyGluGluIleSerIleGlnValSe 293
    | |||||
367| GGTGGATTTTAAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGCTC 318
    | |||||
293| rAsnProSerLeuLeuAspProAspGlnAspAlaThrTyrPheGlyAlaP 310
    | |||||
317| CAACCCCTCCTTACTTGATCCGATCCGATCAGGATGCAACATATCTTTGGGCTT 268
    | |||||
310| heLysValGlnAspIleAsp 316
    | |||||
267| TTAAGTTCGAGATATAGAT 248
    | |||||

seq_name: gb_gss12:AQ827168

seq_documentation_block:
LOCUS   AQ827168          529 bp      DNA           27-AUG-1999
DEFINITION   HS_5256_B2_G09_77A RPCI-11 Human Male BAC Library Homo sapiens
              genomic clone Plate=832 Col=18 Row=N, DNA sequence.
ACCESSION   AQ827168
VERSION     AQ827168.1  GI:5793230
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 529)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 832 row: N column: 18
Seq primer: T7
Class: BAC ends
High quality sequence stop: 529.
location/Qualifiers
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="Plate=832 Col=18 Row=N"
    /clone_lib="RPCI-11 Human Male BAC Library"
    /sex="male"
  /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

BASE COUNT      147 a 121 c 102 g 153 t
ORIGIN

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alignment_scores:
  Quality: 315.50      Length: 82
  Ratio: 4.264        Gaps: 1
  Percent Similarity: 90.244  Percent Identity: 78.049

alignment_block:
US-08-989-362-2 x AQ827168/rev ..
Align seg 1/1 to reverse of: AQ827168 from: 1 to: 529

235 LeuGlnLeuMetValTyrValValLysThrSerIleLysLeuProSerSe 251
    |||||
501 CTTCAACTAATGGTGTGTCACCTA...NACCAGCATCAAAATCGCAAGTTC 455
    |||||
251 rHisAsnLeuMetLysGlySerThrLysAsnTrpSerGlyAsnSerG 268
    |||||
454 TCATACNTGATGAAGGAGCAGCACCAAGTATTGGTCAGGGAATTCGT 405
    |||||
268 luPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgAla 284
    |||||
404 AATTCCATTTTATTCATAAACGTTGTCATTTTCTAAGTTACGGTCT 355
    |||||
285 GlyGluGluLeuSerIleGlnValSerAsnProSerLeuLeuAspProAs 301
    |||||
354 GGAGAGGAAATCAGCATCGAGGTCTCCAAAGCCCTCTTACTGGATCCGA 305
    |||||
301 pGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
    |||||
304 TCAGGATGCAACATACCTTTGGGGCTTTTAAAGTTCGAGATATAGAT 259
    |||||

seq_name: gb_est33:BE042463

seq_documentation_block:
LOCUS   BE042463          618 bp      mRNA           08-JUN-2000
DEFINITION   ho22c06.x1 NCI-CGAP_Col4 Homo sapiens cDNA clone IMAGE:3038122 3'
              similar to SW:TRAI_HUMAN P50591 TNF-RELATED APOPTOSIS INDUCING
              LIGAND ;, mRNA sequence.
ACCESSION   BE042463
VERSION     BE042463.1  GI:8359516
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 618)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 421.
location/Qualifiers
  1..618
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:3038122"
    /clone_lib="NCI-CGAP_Col4"
    /tissue_type="moderately-differentiated adenocarcinoma"
    /lab_host="DH10B"
    /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.

```

FEATURES
source


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LOCUS       AW945165               718 bp    mRNA                    EST           31-MAY-2000
DEFINITION   EST361358  MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
ACCESSION    AW945165
VERSION      AW945165.1  GI:8122916
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 718)
AUTHORS     Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            J.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
TITLE       Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
JOURNAL     Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 0
            Seq primer: Reverse.
            Location/Qualifiers
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="MAGE resequences, MAGA"
                /note="Vector: pbluescriptskm"
BASE COUNT   271 a 136 c 130 g 179 t 2 others
ORIGIN

alignment_scores:
  US-08-989-362-2 x AW945165      ..
  Align seg 1/1 to: AW945165      from: 1 to: 718

183 LeuSerSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMe 198
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
12 ATAACTCTCTGGGAATCATCAAGAGTGGCATTCATTCTCTGAGCACTT 61

198 tThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTrL 215
   : ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 GCATTGTAGGAATGCTGAACTGCTCATCCATGAAAAAGGTTTACTACA 111

215 euTyrAlaAsnIleCysPheArgHisGluThrSerGlySerValPro 231
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
112 TCTATTCCTCAACATACACTTCTTCAGTTCAGGAGGAATAAAGAAACACA 161

232 ThrAspTyrLeuGlnMetValTyrValLysThrSerIleLysIle 248
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
162 AGAACGCAACAACAAATGCTCAATATATTACAAATACACA...AGTTA 208

248 eProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerG 265
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
209 TCCTGACCCCTATATTCTTCAATGAAAGTCTAGAAATAGTTGTGCTCA 258

265 lYasnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLys 281
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
259 AGATGTCAGAAATATGACACTCTATTCCATCTATCAAGGGGGAATATTGAG 308

282 LeuArgAlaGlyGluGluThrSerIleGlnValSerAsnProSerLeuLe 298
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
309 CTTAAGGAAATGACAGAAATTTTGTCTCTGAACAAATGACGACACTTGAT 358

298 uAspProAspGlnAspAlaThrTyrPheGlyAlaPheLysVal 312
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seq_name: gb_gss11:AQ817650

seq_documentation_block:
  LOCUS       AQ817650               413 bp    DNA                    GSS           26-AUG-1999
  DEFINITION   HS_5265_B1_D03_SpeE RPCI-11 Human Male BAC Library Homo sapiens
              genomic clone Plate=841 Col=5 Row=H, DNA sequence.
  ACCESSION    AQ817650
  VERSION      AQ817650.1  GI:5780043
  KEYWORDS     GSS.
  SOURCE       human.
  ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE   1  (bases 1 to 413)
  AUTHORS     Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
              Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
              Hood,L.
  TITLE       Sequence-tagged connectors: A sequence approach to mapping and
              scanning the human genome
  JOURNAL     Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE     99380589
  COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
              High Throughput Sequencing Center
              University of Washington
              401 Queen Anne Avenue North, Seattle, WA 98109, USA
              Tel: (206) 616-3618
              Fax: (206) 616-3887
              Email: jwallace@u.washington.edu
              Clones are derived from the human BAC library RPCI-11. For BAC
              library availability, please contact Pieter de Jong
              (pieter@dejong.med.buffalo.edu). Clones may be purchased from
              BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
              or from Resear h Genetics (info@resgen.com). BAC end Web Server:
              http://www.htsc.washington.edu
              Plate: 841 row: H column: 5
              Seq primer: SP6
              Class: BAC ends
              High quality sequence stop: 413.
              Location/Qualifiers
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                  /db_xref="taxon:9606"
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                  /clone_lib="RPCI-11 Human Male BAC Library"
                  /sex="male"
                  /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                  Male blood DNA was isolated from one randomly chosen donor
                  and partially digested with a combination of EcoRI and
                  EcoRI Methylase. Size selected DNA was cloned into the
                  pBACe3.6 vector at EcoRI sites"
BASE COUNT   108 a 82 c 100 g 123 t
ORIGIN

alignment_scores:
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  Align seg 1/1 to: AQ817650      from: 1 to: 413

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   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 TCTGAATTCATTTTATTCATTAACCTTGGCGGATATTTAAGTTACG 54

283 gAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspP 300
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55 GTCTGGAGAGAAATCATCATCGAGGCTCTCCAAACCCCTCTTACTGGATC 104

300 roAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspLeasp 316
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105 CCGATCAAGATGCAACATCTTTGGGGCTCTTAAGAGCGAGATATGGAT 154

seq_name: gb_est20:AW104819

seq_documentation_block: 585 bp mRNA EST 20-OCT-1999
LOCUS AW104819
DEFINITION x57b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597851 3'
similar to SW:TRAI_HUMAN P50591 TNF-RELATED APOPTOSIS INDUCING
LIGAND /, mRNA sequence.

ACCESSION AW104819
VERSION AW104819.1 GI:6075554
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 585)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco
High quality sequence stop: 405.
Location/Qualifiers
1. .585
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/db_xref="taxon:9606"
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/lab_host="DH10B"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

BASE COUNT 146 a 111 c 105 g 221 t 2 others
ORIGIN

alignment_scores:
Quality: 206.00 Length: 132
Ratio: 2.264 Gaps: 3
Percent Similarity: 68.939 Percent Identity: 35.606

alignment_block:
US-08-989-362-2 x AW104819/rev ..

Align seg 1/1 to reverse of: AW104819 from: 1 to: 585

183 LeuSerSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMe 198
:|||||
552 ATAACCTNTGGTCAATCAAGAGTGGGATTCATCTCCGTGAGCAACT 503
198 tThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTrL 215
: ||| |||||
502 GCACCTTGAGGAATGGTGAATGCTGCATCCATCCAGAAAGGGTTTACTACA 453

215 euTyrAlaAsnIleCysPheArgHisGluThrSerGlySerValPro 231
:|||||
452 TCATTCCCAACATACCTTTCGATTTCCAGGAGAAATAAAGAAACACA 403
232 ThrAspTyrLeuGlnIleMetValTyrValLysThrSerIleLysI 248
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402 AAGAAGCAGACAACAAATGGTCCAATATATTACAAATACACA...AGTTA 356
248 eProSerSerHisAsnLeuMetLysGlySerThrLysAsnTrpSerG 265
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355 TCCTGACCCCTATATGTTGATGAAAGTCTAGAAATAGTTGTTGGTCTA 306
265 lyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePhe 281
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305 AAGATCAGAATATGGACTCTATTCCATCTATCAAGGGGGAATATTGAG 256
282 LeuArgAlaGlyGluGlnIleSerIleGlnValSerAsnProSerLeu 298
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255 CTTAAGGAAATACAGAAATTTTGTCTCTAACAATGAGCAGCTTGAT 206
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205 AGACATGGACCATGACAGCCAGTCTTTTCGGGGCCTTTTAGTT 162

seq_name: gb_est32:BE005955

seq_documentation_block: 604 bp mRNA EST 05-JUN-2000
LOCUS BE005955
DEFINITION RCO-BN0121-210300-031-e03 BN0121 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE005955
VERSION BE005955.1 GI:8266188
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 604)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=RC0-BN0121-210300-031-e03&t3=2000-03-21&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 29
High quality sequence stop: 164.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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FEATURES
source

[illegible]


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127 GlnLysGluLeuGlnHisIleValGlyProGlnArgPheSerGlyAlaPr 143
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348 AGAAAGAAAGCAACAAATATTTCTCCCTA..... 317
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143 oAlaMetMetGluGlySerTrpLeuAspValAlaGlnArgGlyLysProG 160
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316 .....GTGAGAGAAAGAGGCTCTCAG 295
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160 luAlaGlnProPheAlaHisLeuThr.....IleAsnAla 171
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294 GAGTAGCA.....GCTCATACTGGGACCAGGAGGAAGCAACACA 251
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172 AlaSerIleProSerGlySerHisLysValThrLeu.....Se 184
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250 TTGTCTTCTCCAACTCCAAGATGAAAGGCTCTGGGCCCAAAATAA 201
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184 rSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMetThrL 200
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